

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 22, 2003, 15:17:40 ; Search time 69 Seconds

(without alignments)

570.496 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272

Sequence: 1 MEGTSPFDSQSASRNKWSY.....LIIMKNASEKEKKKKRRN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03.\*

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23:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	688.5	54.1	213	22	Testis Enhanced Ge
2	499.5	39.3	140	22	Testis Enhanced Ge
3	498.5	39.2	138	21	Arabidopsis thalia
4	498.5	39.2	154	21	Arabidopsis thalia
5	495	38.9	110	21	Arabidopsis thalia
6	492.5	38.7	129	21	Arabidopsis thalia
7	491.5	38.6	236	22	Arabidopsis thalia
8	483.5	38.0	255	21	Rovine mammary tis
9	477.5	37.5	237	19	Lung cancer associ
					Bax inhibitor BI-1

10	331.5	26.1	245	23	ABP42996
11	324	25.5	277	22	AAU30218
12	312	24.5	245	22	ABB63069
13	192	15.1	305	22	ABB57985
14	172	13.5	341	22	ABB58798
15	171	13.4	346	21	AAAG49311
16	166	13.1	122	21	AAG03753
17	165	13.0	242	22	AAB64490
18	165	13.0	345	20	AAW81998
19	165	13.0	345	21	AAW79139
20	165	13.0	345	21	AAW66631
21	165	13.0	345	21	AAW59435
22	165	13.0	345	22	AAB65154
23	165	13.0	345	23	ABP61812
24	165	13.0	345	23	ABG34030
25	165	13.0	345	23	ABB89838
26	165	13.0	345	24	ABP71505
27	165	13.0	345	24	ABU59047
28	165	13.0	345	24	ABU59194
29	165	13.0	345	24	ABU59343
30	165	13.0	345	24	ABU60478
31	165	13.0	345	24	ABU57969
32	165	13.0	345	24	ABU58900
33	165	13.0	345	24	ABU13860
34	165	13.0	345	24	ABU10815
35	165	13.0	346	19	AAW74901
36	165	13.0	346	23	ABG95353
37	165	13.0	351	20	AAW76620
38	165	13.0	351	21	AAW43975
39	143.5	11.3	250	22	AAB64489
40	132	10.4	319	21	AAW83263
41	128.5	10.1	241	20	AAW37315
42	123	9.7	290	21	AAW33365
43	123	9.7	324	22	ABG60180
44	121	9.5	227	24	ABP77220
45	118.5	9.3	221	21	AAW33367

## ALIGNMENTS

## RESULT 1

AAW65755  
ID AAB65755 standard; Protein; 213 AA.

XX  
AC AAB65755;

XX  
DT 27-MAR-2001 (first entry)

XX  
DE Testis Enhanced Gene Transcript protein #1.

XX  
KW Cell death modulator; programmed cell death; apoptosis;  
forestry plant.

XX  
OS Pinus radiata.

XX  
PN WO200075331-A1.

XX  
PD 14-DEC-2000.

XX  
PF 02-JUN-2000; 2000WO-NZ00086.

XX  
PR 04-JUN-1999; 99US-0325932.

XX  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
(FLET-) FLETCHER CHALLENGE FORESTS LTD.

XX  
PI Flinn B, Lasham A;

XX  
WPI; 2001-061724/07.

XX  
N-PSDB; AAF44782.

XX  
PT Novel defender against cell death polynucleotide useful for modulating

PT programmed cell death pathway and specific development pathways in  
PT forestry plant -

XX Claim 22; Pages 81-82; 142pp; English.

XX The present invention relates to coding sequences (see AAF44740-F44840  
CC and AAF4843-F44844) and proteins (see AAB65714-B65814) involved in  
CC programmed cell death (PCD; apoptosis). The coding sequences and proteins  
CC of the present invention are useful for modulating a PCD or cell death  
CC pathway and various developmental pathways in a forestry plant, by  
CC stably incorporating one of the present coding sequences into the genome  
CC of the forestry plant, where the coding sequence provides a PCD pathway  
CC that is not present in a native form of the forestry plant.

XX SQ Sequence 213 AA;

Query Match 54.1%; Score 688.5; DB 22; Length 213;  
Best Local Similarity 64.6%; Pred. No. 3.9e-73;  
Matches 137; Conservative 31; Mismatches 41; Indels 3; Gaps 2;

QY 39 QVYLTLCCALVSAAGAYLHILWNIGLLTTMACMGSMVWLLSAP--PQEQKRVALLMA 96  
Db 1 RVLVSUSCALVTAAGVYLHLLNLNIGLLTGLACIGSVIGLLSVPTSSNNEGKRAALLA 60

QY 97 AALFEGASIGPLIELGINFDPSTVFGAFVGCFAAAMLARRELYLGLSSG 156  
Db 61 AAFKATGLPLIDAVINDSSILVSAFVGTSLAFACFAAATARRRELYLGLSSG 120

QY 157 VSLFLWLFHFASSIFGSGMAVFKFELYFGLLVFVGYIVFDQTQETIEKAHGLDMDYVKHALT 216  
Db 121 ISILMLQLASSIFGSGSAIYTFEIVFGLLVFGLYIIFDQMIETAKDGDYDYLKHSLD 180

QY 217 LFTDFGAVFVRLIILMKNKNA-SEKEKKKKRR 247  
Db 181 LFTDFVAVFVRLVIMAKNADSKSREGKKRR 212

RESULT 2  
AAB65756  
ID AAB65756 standard; Protein; 140 AA.

XX AAB65756;

XX 27-MAR-2001 (first entry)

XX Testis Enhanced Gene Transcript protein #2.

XX Cell death modulator; programmed cell death; PCD; apoptosis;  
KW forestry plant.

XX Pinus radiata.

XX WO200075331-A1.

XX 14-DEC-2000.

XX 02-JUN-2000; 2000WO-NZ00086.

XX 04-JUN-1999; 99US-0325932.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.

XX Flinn B, Lasham A;

XX WPI; 2001-061724/07.

XX N-PSDB; AAF44783.

XX Novel defender against cell death polynucleotide useful for modulating  
PT programmed cell death pathway and specific development pathways in  
PT forestry plant -

XX Claim 22; Page 82; 142pp; English.

XX The present invention relates to coding sequences (see AAF44740-F44840  
CC and AAF4843-F44844) and proteins (see AAB65714-B65814) involved in  
CC programmed cell death (PCD; apoptosis). The coding sequences and proteins  
CC of the present invention are useful for modulating a PCD or cell death  
CC pathway and various developmental pathways in a forestry plant, by  
CC stably incorporating one of the present coding sequences into the genome  
CC of the forestry plant, where the coding sequence provides a PCD pathway  
CC that is not present in a native form of the forestry plant.

XX SQ Sequence 140 AA;

Query Match 39.3%; Score 499.5; DB 22; Length 140;  
Best Local Similarity 66.2%; Pred. No. 6.2e-51;  
Matches 100; Conservative 14; Mismatches 26; Indels 11; Gaps 2;

QY 1 MEGTGFQFSQASARNRWSYDSLKNFRQISPLYOTHLKOVYLTCCALVASAAGAYLHL 60  
Db 1 MDAFASLFQS---SGKWSHSDSLKNFRQISPAVQSHLKNVYLSLCCALMASAGAYLHLM 57

QY 61 WNTGGLTTMACMGSMVWLLSAPPYQEQKRVALLMAALFEGASIGPLIELGINFDPSTV 120  
Db 58 LNIIGLLTTIACIGSVIWLISIPPHBEQKRFGLMAAALFEGACIGPLIEAALKVDPSTV 117

QY 121 FGAFCVCAVFGCFSAAMLARRELYLGG 151  
Db 118 ISAFVGSALAFACFSGAA-----CWLGG 140

RESULT 3  
AAG19970  
ID AAG19970 standard; Protein; 138 AA.

XX AAG19970;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 21975.

XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 28-APR-1999; 99US-0130891.

XX 30-APR-1999; 99US-0131449.

XX 30-APR-1999; 99US-0132048.

XX 04-MAY-1999; 99US-0132407.

XX 06-MAY-1999; 99US-0132484.

XX 06-MAY-1999; 99US-0132485.

XX 06-MAY-1999; 99US-0132486.

XX 07-MAY-1999; 99US-0132487.

XX 07-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134376.  
PR 19-MAY-1999; 99US-0134768.  
PR 20-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
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PR 18-JUN-1999; 99US-0139461.  
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PR 18-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
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PR 31-AUG-1999; 99US-0151303.  
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PR 07-SEP-1999; 99US-0151930.  
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PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
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PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 39.2%; Score 498.5; DB 21; Length 138;

Best Local Similarity 70.5%; Pred. No. Be-51;

Matches 91; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MEGFTSFDSQASNRNWSYSLKRFQISPLVQTHLKVYLTCCALVASAGAYLHL 60

DB 1 MDAFSFDSOPGSRK-WSYSLKRFQISPAVQNHKRVYLTCCALVASAGAYLHL 59

QY 61 WNIGILLTMACGMWVLLSAPPYQEQKRVALLMAALFEAGSIGPLIEIGINFDPISIV 120

DB 60 WNIGILLTIGIGTMIWLLSPPYEHQKRLSLFASAVLEGASVGLIKVAIDVDPSTL 119

QY 121 FGAFFGCAV 129

DB 120 ITAFVGTAI 128

#### RESULT 4

AAAG19969  
ID AAG19969 standard; Protein; 154 AA.

XX AC AAG19969;

XX AC AAG19969;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 21974.

XX KW Protein identification; signal transduction pathway; metabolic pathway;

XX KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX KW termination sequence.

XX OS Arabidopsis thaliana.

XX XX EP1033405-A2.

XX XX 06-SEP-2000.

XX XX 25-FEB-2000; 2000EP-0301439.

XX XX 25-FEB-1999; 99US-0121825.

XX XX 05-MAR-1999; 99US-0123180.

XX XX 09-MAR-1999; 99US-0123548.

XX XX 23-MAR-1999; 99US-0125788.

XX XX 25-MAR-1999; 99US-0126264.

XX XX 29-MAR-1999; 99US-0126785.

XX XX 01-APR-1999; 99US-0127462.

XX XX 06-APR-1999; 99US-0128234.

XX XX 08-APR-1999; 99US-0128714.

XX XX 16-APR-1999; 99US-0129845.

XX XX 19-APR-1999; 99US-0130077.

XX XX 21-APR-1999; 99US-0130449.

XX XX 23-APR-1999; 99US-0130510.

XX XX 28-APR-1999; 99US-0130891.

XX XX 30-APR-1999; 99US-0131449.

XX XX 30-APR-1999; 99US-0132048.

XX XX 04-MAY-1999; 99US-0132484.

XX XX 05-MAY-1999; 99US-0132485.

XX XX 06-MAY-1999; 99US-0132486.

XX XX 06-MAY-1999; 99US-0132487.

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PR 14-MAY-1999; 99US-0134221.  
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PR 18-MAY-1999; 99US-0134768.  
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PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
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PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
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PR 08-JUL-1999; 99US-0142803.  
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PR	22-OCT-1999;	99US-0160980;
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PR	22-OCT-1999;	99US-0160989;
PR	25-OCT-1999;	99US-0161404;
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PR	28-OCT-1999;	99US-0161992;
PR	28-OCT-1999;	99US-0161993;
PR	29-OCT-1999;	99US-0162142;
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Best Local Similarity 39.2%;		
Matches 91; Conservative 2		
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DB	17	MDAFSSFFDSQGSRS-WS
QY	61	WNIGGLITTMACMSMWHL
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QY	121	FGAFVGCAY 129
DB	136	ITAFVGTAI 144
RESULT 5		
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XX	AC	AAG19971;
XX	DT	17-OCT-2000 (first entry)
XX	DE	Arabidopsis thaliana protein
XX	KW	Protein identification; sign
KW	KW	hybridisation assay; genetic
KW	XX	termination sequence.
XX	OS	Arabidopsis thaliana.
PN	EP1033405-A2.	
XX	PD	06-SEP-2000.
XX	PF	25-FEB-2000; 2000EP-0301439.
XX	XX	
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PR	05-MAR-1999;	99US-01231825;
PR	09-MAR-1999;	99US-0123180;
PR	23-MAR-1999;	99US-0123548;
PR	23-MAR-1999;	99US-01235788;
PR	23-MAR-1999;	99US-0126264;
PR	29-MAR-1999;	99US-0126785;
PR	01-APR-1999;	99US-0127462;
PR	06-APR-1999;	99US-0128234;
PR	08-APR-1999;	99US-0128714;
PR	16-APR-1999;	99US-0129845;
PR	19-APR-1999;	99US-0130077;
PR	21-APR-1999;	99US-0130449;
PR	23-APR-1999;	99US-0130510;
PR	23-APR-1999;	99US-0130891;
PR	28-APR-1999;	99US-0131449;
PR	30-APR-1999;	99US-0132048;
PR	30-APR-1999;	99US-0132407;
PR	04-MAY-1999;	99US-0132484;
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Query Match 39.2%; Score 498.5; DB 21; Length 154;

Best Local Similarity	70.5%	Pred. No.	9.3e-51;

Matches 91; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

[illegible]

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76 WNTGGII TTIGCIGCTMTWIL SCBPBYEHOKPISLIFASAVIECASVCPI TKVAITDVDBSI 135

0v 121 FGAEVGCAY 129

Detailed description of Figure 1: This is a Western blot image. On the left, molecular weight markers are labeled in kilodaltons (kDa): 116, 97.4, 72, 66, 55, 43, 36, 29, 25, 21, 14.6, and 12. The blot has four lanes. The first lane is labeled 'Control'. The second lane is labeled 'Doxorubicin'. The third lane is labeled 'Doxorubicin + Curcumin'. The fourth lane is labeled 'Doxorubicin + Curcumin + Curcumin'. There are three rows of bands. The top row is labeled 'p53' on the right. The second row is labeled 'p21' on the right. The third row is labeled 'GAPDH' on the right. In the 'Control' lane, p53 and p21 bands are faint. In the 'Doxorubicin' lane, p53 and p21 bands are significantly more intense. In the 'Doxorubicin + Curcumin' lane, the p53 and p21 bands are less intense than in the 'Doxorubicin' lane. In the 'Doxorubicin + Curcumin + Curcumin' lane, the p53 and p21 bands are very faint, similar to the 'Control' lane. GAPDH bands are of similar intensity across all four lanes, indicating equal protein loading.

D<sub>b</sub> 136 ITAFVGTAI 144

## RESULT 5

AAG19971

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ID AAGT99/I

AC AAG19971;

[illegible]

17-OCT-2000 (first entry)  
 B1  
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 21976

XX

**KW** Protein identification; signal transduction pathway; metabolic pathway;  
**KW** hybridisation assay; genetic mapping; gene expression control; promoter

KW	termination assay,
KW	termination sequence

XX

OS Arabidopsis thaliana  
YY

PN EP1033405-A2.

XX

PD 06-SEP-2000.  
yy

25-FEB-2000; 2000EP-0301439.

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PR 05-MAR-1999; 99US-0123180

PK 03-MAR-1993; 3303-0123180.  
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PK 29-MAR-1999; 99US-0126783;  
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PR 06-APR-1999; 99US-0128234.

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PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
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PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 38.9%; Score 495; DB 21; Length 110;
Best Local Similarity 86.4%; Pred. No. 1.5e-50;
Matches 95; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

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QY 199 IIEKAHLGDMYVYKHALTFTDFGAVFVRILITMLKNAKEKKKKRRN 248
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Db 61 IIEKAHLGDMYVYKHALTFTDFGAVFVRILITMLKNAKEKKKKRRN 110

RESULT 6
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AC AAG54829;
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XX 18-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 70059.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
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Query Match 38.7%; Score 492.5; DB 21; Length 129;
Best Local Similarity 71.4%; Pred. No. 3.8e-50;
Matches 90; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

QY 1 MEGTFFDSSASRNWSYDSLKFNFRQISPLIVOTHLKQVYILCCALVASAGAYLHIL 60
Db 1 MDAFFSFFDSQPGSRs-WSYDSLKFNFRQISPAVONHLKRYLTLCCALVASAFAYLHVL 59
QY 61 WNIGGLTITMACGMVWLLSAPPYQOKRVALLMAALFEGASIGPLIELGNFDPsIV 120
Db 60 WNIGGLTITGICIGTMIWLLSCPPYEHQKRLSLFASVLEGSVGLKXVALDVDPsIL 119
QY 121 FGAFVG 126
Db 120 ITAFVG 125

RESULT 7
AAB87615
ID AAB87615 standard; protein; 236 AA.
XX
AC AAB87615;
XX
DT 15-MAY-2001 (first entry)
XX
DE Bovine mammary tissue derived protein #6.
XX
KW Bovine; mammary gland; cancer; tumour; angiogenesis.
XX
OS Bos taurus.
XX
PN WO200114553-A1.
XX
PD 01-MAR-2001.
XX
PF 23-AUG-2000; 2000WO-NZ00166.
XX
PR 23-AUG-1999; 99US-0150330.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.
PI Havukkala LJ, Gleen M, Grigor MR, Molenaar AJ;
XX WPI; 2001-226619/23.
XX
PT New polypeptides and polynucleotides encoding the polypeptides, which
PT are expressed in bovine mammary gland tissue, useful for stimulating
PT mammary gland growth or function, or inducing differentiation of milk
PT producing cells -
XX
PS Claim 11; Page 62; 97pp; English.
XX
CC The present invention relates to proteins derived from bovine
CC mammary gland cells. The invention is useful for stimulating
CC bovine mammary gland cell growth and function, inhibiting the
CC growth of various mammary gland cancer cells, inhibiting
CC angiogenesis and vascularization of tumours, or modulating
CC the growth of blood vessels in a mammal.
XX
XX Sequence 236 AA;
```



PI	Reed JC, Xu Q;	KW
XX		KW
XX	WPI; 1998-531519/45.	KW
DR	N-PSDB; AAV59067.	KW
XX		KW
PT	Bax inhibitor proteins, BI-1 and BI-2 - useful e.g. to modulate	KW
PT	cellular apoptotic activity or identify agents altering BI-1 or BI-2	XX
PT	binding which can modulate apoptotic activity	OS
XX		XX
PS	Claim 14; Fig 1; 80pp; English.	XX
PS		PN

...treatment and diagnosis of cancer (e.g.,

tumors, cardiovascular disorders and

2200: English

[illegible]

2008 031 E. 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1590 1591 1592 1593 1594 1595 1596 1597 1598 1599 1600 1601 1602 1603 1604 1605 1606 1607 1608 1609 1610 1611 1612 1613 1614 1615 1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1700 1701 1702 1703 1704 1705 1706 1707 1708 1709 1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731 1732 1733 1734 1735 1736 1737 1738 1739 1740 1741 1742 1743 1744 1745 1746 1747 1748 1749 1750 1751 1752 1753 1754 1755 1756 1757 1758 1759 1760 1761 1762 1763 1764 1765 1766 1767 1768 1769 1770 1771 1772 1773 1774 1775 1776 1777 1778 1779 1780 1781 1782 1783 1784 1785 1786 1787 1788 1789 1790 1791 1792 1793 1794 1795 1796 1797 1798 1799 1800 1801 1802 1803 1804 1805 1806 1807 1808 1809 1810 1811 1812 1813 1814 1815 1816 1817 1818 1819 182

Pred. No. 1.2e-30;

[illegible]

UDDNTSHITTFSTIQUBERKVIASOFALGCMFVAFAGRIVHMVTH / 0

..SAPPYQ--EQKRVALLMAAALEFGASIGPLIELGINFDPS I18

2008 031 E. 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1590 1591 1592 1593 1594 1595 1596 1597 1598 1599 1600 1601 1602 1603 1604 1605 1606 1607 1608 1609 1610 1611 1612 1613 1614 1615 1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1700 1701 1702 1703 1704 1705 1706 1707 1708 1709 1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731 1732 1733 1734 1735 1736 1737 1738 1739 1740 1741 1742 1743 1744 1745 1746 1747 1748 1749 1750 1751 1752 1753 1754 1755 1756 1757 1758 1759 1760 1761 1762 1763 1764 1765 1766 1767 1768 1769 1770 1771 1772 1773 1774 1775 1776 1777 1778 1779 1780 1781 1782 1783 1784 1785 1786 1787 1788 1789 1790 1791 1792 1793 1794 1795 1796 1797 1798 1799 1800 1801 1802 1803 1804 1805 1806 1807 1808 1809 1810 1811 1812 1813 1814 1815 1816 1817 1818 1819 182

Pred. No. 1.2e-30;

[illegible]

UDDNTSHITTFSTIQUBERKVIASOFALGCMFVAFAGRIVHMVTH / 0

..SAPPYQ--EQKRVALLMAAALEFGASIGPLIELGINFDPS I18

71 FTQAGLLSGLIIMWIMTPSHETEQKRLGLAGFAFLTCVGLGPALEECIAVNP 130  
Db  
119 IVFGAFVCGAVVFGCSAAAMLARRRYLIGLLSGSVLLFLWHFASIFGSMVAFK 178  
QY  
131 ILPTAFMTAMITCTFTSALYARRRSLYFLGLGIMSPPELGAFASLGNQFF- 189  
Db  
179 FELYFGLLVFVGVIYVFDTQETIEKAHL 205  
QY  
190 ANLYXGLVVMGGAFLILNSLKKPNM 216  
Db

RESULT 11  
AAU30218  
ID AAU30218 standard; Protein; 277 AA.

XX  
DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #709.

XX	Human; vaccination; gene therapy; nutritional supplement;
KW	stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW	immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX	
OS	Homo sapiens.

AA  
PN  
WO200179449-A2.

25-OCT-2001.

PF 16-APR-2001; 2001WO-US08656.

PR 18-APR-2000; 2000US-0552929.

XX  
XX

09T07-0-00T00Z, T00Z NNN 07  
BT

PI Tang YT, Liu C, Drmanac RT;  
XX (NAME) MICRO INC.

DR WPI; 2001-611725/70.

Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -

PS Claim 20; Page 262; 765pp; English.

The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.

Sequence 277 AA;

Query Match	25.5%	Score 324;	DB 22;	Length 277;
Best Local Similarity	35.0%;	Pred. No. 1.1e-29;		
Matches	93;	Conservative 51;	Mismatches 88;	Indels 3

QY 3 GETSFDSASRNRWSYDLKNFRQISPLV-QTHLKQVYLTLCCALVASAGAYLHLW 61

```

Db      17  GTMNFD-----RKITFDALLKFSHTIPSTQQAHHKKVYASFALCYFGAAGAVNNMT 70
QY      62  NI--GGLTTMACMGSMVWLLSAPPYQ--EOKRV--ALLMAALFEGASIGPLI--ELG 112
Db      71  HFIAQGLLSALGSLILMLWLMATPHSHETQEKRLCTSLLGFCIYRKLGLGPAIGSFVIA 130
QY      113  INFDPISVFGAFVCCA--VVGCFPSAAAMLAR--REYLYLGGLLSGVSL--FWLHFASSI 169
Db      131  VKRQASLP-TAFMGHSGNSGSPAFTLSALLCRPRSYFLGGLTMSALSALVAFCLPLGNVF 189
QY      170  FGGSMAYFKELYEGLVFVGYIVEDTQEIIEKAHLGDMDY--VKHALTLFTDFGAVFRI 228
Db      190  FWFPFWFQANLYVGLVVMCGVFLFDQLIIIEKAEGQGDQYNLWHCIDLFDLDTITVF--- 246
QY      229  LIIMLKNASE-----KEEKKKKRN 248
Db      247  ----QKNSMKDPGPXMKKKKKKRN 268

```

RESULT 12  
ABB63069

ID ABB63069 standard; Protein; 245 AA.

AC ABB63069;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 15999.

Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

05 Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

23-MAR-2000; 2000US-191637P.

FR 11 JUL 2000; 2000US-0614150.  
XX

PA (PEKE) PE CORP NY

PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI; 2001-656860/75.

DR N-PSDB; ABL07172.

PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from *Drosophila* and for elucidating cell signalling and cell-cell  
PT interactions -

PS Disclosure; SEQ ID NO 15999; 21pp + Sequence Listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from *Drosophila*. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA sequences (ABU101840-ABU16175) and the encoded proteins (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at [ftp.wipo.int/pub/published/pct\\_sequences](http://ftp.wipo.int/pub/published/pct_sequences).

AA	Sequence	245 AA;
SQ		

Query Match	24.5%;	Score 312;	DB 22;	Length 245;
Best Local Similarity	34.4%;	Pred. No. 2.5e-28;		
Matches 77; Conservative	48;	Mismatches 83;	Indels 18;	Gaps 5;





```

Db      132 CVLTAAARATFRSHRLELASGGIATIASALVTGSAVARSIYQGLGAKHLAWA 191
QY      95 MAALFEGASIGPLIEIGINFDPISIVFAGVGCFAVVGCFSAAMLARREYLYLGGLLSSG 156
Db      192 VHCAIL-GAVIAPICFEG---GPIITRAALYTGGIV-GGLSTIAACAPSKDFLYMGGLA 246
QY      155 SGVSLLF-----WLHFASISFGGMAVFKFELYFGLLVFVGIVYIVFDTOEITEKAHL-- 205
Db      247 IGLGVFVFASSIASMWLPPTTALGAG---LASMSLYGGLVLFSGFLLYDTORMVRRAEVYP 303
QY      206 ---GMDYVVKHALTLFTDFGAVFVRILIM 232
Db      304 QYSYTPDPINASMSIYMDVINIFIRLVTL 334

```

## RESULT 15

AA49311  
 AAB49311 standard; Protein; 346 AA.

XX AC AAB49311;

XX DT 01-MAR-2001 (first entry)

XX DE Mouse brown adipose tissue clone 42 protein.

XX KW Growth hormone; brown adipose tissue.

XX OS Mus sp.

XX PN W0200066784-A2.

XX PD 09-NOV-2000.

XX PF 05-MAY-2000; 2000WO-US12145.

XX PR 05-MAY-1999; 99US-0132670.

XX PA (UYOH-) UNIV OHIO.

XX PI Kopchick JJ, Li Y;

XX PS WPI; 2000-665338/64.

XX PT Diagnosis of abnormal levels of growth hormone in brown adipose tissue  
 PT is carried out by monitoring the transcriptional activity of one or  
 PT more genes related to growth hormone activity -

PS Disclosure; Page 66; 89pp; English.

XX The present invention provides a method of diagnosing abnormal levels of  
 CC growth hormone (GH) in brown adipose tissue, by assaying the levels of  
 CC specific gene transcripts. The genes of interest are those encoding  
 CC glucosephosphate isomerase, neuroleukin, pyruvate kinase, haem oxygenase,  
 CC ubiquitin/ribosomal fusion protein, alpha-enolase, proteasome theta  
 CC chain, trans-Golgi network protein, medium chain acyl-CoA dehydrogenase,  
 CC adipocyte lipid binding protein, mitochondrial cytochrome C oxidase,  
 CC mitochondrial NADH-ubiquinone oxidoreductase, mitochondrial cytochrome B  
 CC or any of the genes Ng-119K42, Ng-119K45, Ng-119K36, Ng-119K62,  
 CC Ng-119K42, Ng-119K58, Ng-119K65 or Ng-119K66. This is useful for  
 CC diagnosing abnormal levels of GH or predicting changes in brown adipose  
 CC tissue.

XX SQ Sequence 346 AA;

Query Match 13.4%; Score 171; DB 21; Length 346;

Best Local Similarity 25.9%; Pred. No. 2.2e-11;

Matches 57; Conservative 47; Mismatches 84; Indels 32; Gaps 9;

QY 42 LTLCALVASRAGAYLHIL----W-NIGGLITMACGSMVWLLSAPPYQOKRVAILMA 96

Db 138 LTALSALAVARTPALMNFMTGWSVYTIATFAAMIGAGMLVHSISYEQSGPKHLAWMLH 197

```

QY      97 AALFEGASIGPLIEIGINFDPISIVFAGVGCFAVVGCFSAAMLARREYLYLGGLLSSG 156
Db      198 SGVM-GAVVAPLITIG--GPIITRAALYTGGIV-GGLSTIAACAPSKDFLYMGGLA 252
QY      157 VSLLFWLHFASISFGGSM-----AVKFKELYFGLLVFVGIVYIVFDTOEITEKAHLG 206
Db      253 LGLV----FASLL--GSMFLPPTSVAGATLYSVAMYGGLVLFSGFLLYDTQKVIKRAEIT 306
QY      207 DM-----DYVKHALTLFTDFGAVFVRILIMLKNASEKE 240
Db      307 PMYGAQKYDPINSMILYIYMDTLNIFMRVATMLATGSRKK 346

```

Search completed: September 22, 2003, 15:23:10  
 Job time : 71 secs

RESULT 2  
US-09-325-932A-88  
; Sequence 88, Application US/09325932A  
; Patent No. 6451604  
; GENERAL INFORMATION:  
; APPLICANT: Flinn, Barry  
; APPLICANT: Lasham, Annette  
; TITLE OF INVENTION: Compositions affecting programmed cell  
; TITLE OF INVENTION: death and their use in the modification of forestry plant des

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; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325.932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 88
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-325-932A-88

Query Match          39.3%; Score 499.5; DB 4; Length 140;
Best Local Similarity 66.2%; Pred. No. 6.4e-51;
Matches 100; Conservative 14; Mismatches 26; Indels 11; Gaps 2;

QY 1 MEGTFPDSQASRNWSDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHL 60
DB 1 MDAFASLFQS---SGKGWSDSLKNFRQISPAVQSHLKNVYLSLCCALMASAGGAYLHLM 57
QY 61 WNIGGLTTMACGSMWNWLLSAPPYQEQKRVALLMAAALFEGASIGPLIEGINFDP 120
DB 58 LNIIGLLTTIACIGSIWLLSIPPEQKRGFLMAAALFEGACIGPLIEAIAIKVDP 117
QY 121 FGAFGCAVFGCGFSAAMLARRREYLYLGG 151
DB 118 ISAFVGSALAFACFSGAA-----CWLGG 140

RESULT 3
US-08-818-514-3
; Sequence 3, Application US/08818514
; Patent No. 5837838
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Xu, Qunli
; TITLE OF INVENTION: BAX Inhibitor Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,514
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-818-514-3

Query Match          37.5%; Score 477.5; DB 2; Length 237;
Best Local Similarity 42.2%; Pred. No. 5.2e-48;
Matches 98; Conservative 53; Mismatches 74; Indels 7; Gaps 4;

QY 19 SYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHLWNTI--GGLLTTMACGSM 76
DB 9 NFDALLKFSHTPTSTQOHLKQVYASFAALCMFYAAGAYVHVHTFTQAGLLSALGSLIM 68
QY 77 VWLLSAPPYQ--EQKRVALLMAAALFEGASIGPLIEGINFDPISIVFGAVGCVF 134
DB 69 IWLMTATPHSHETEOKKGLLAGFAFLTGIGLPALEFCIAVNPISILPTAFMGTA 128
QY 135 SAAMLARREYLYLGGLLSSGVSLFLFWLHFPAASSIFGSGMAVFKFELFGLLV 194
DB 129 TLSALYARRRYSYLFGLGILMSALL--LSSLGNVFFGSIWLFQANLVGVLMCGF 187
QY 195 DTQETIEKAHLGDMYVKAHLTFLTFDGAVFVRILIMLKNASKEEKKKKR 246
DB 188 DTQLLIERAEGDQDIWHCIDLDFITVFKLMMILAMN--EKDKKKKK 237
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DB 9 NFDALLKFSHTPTSTQOHLKQVYASFAALCMFYAAGAYVHVHTFTQAGLLSALGSLIM 68
QY 77 VWLLSAPPYQ--EQKRVALLMAAALFEGASIGPLIEGINFDPISIVFGAVGCVF 134
DB 69 IWLMTATPHSHETEOKKGLLAGFAFLTGIGLPALEFCIAVNPISILPTAFMGTA 128
QY 135 SAAMLARREYLYLGGLLSSGVSLFLFWLHFPAASSIFGSGMAVFKFELFGLLV 194
DB 129 TLSALYARRRYSYLFGLGILMSALL--LSSLGNVFFGSIWLFQANLVGVLMCGF 187
QY 195 DTQETIEKAHLGDMYVKAHLTFLTFDGAVFVRILIMLKNASKEEKKKKR 246
DB 188 DTQLLIERAEGDQDIWHCIDLDFITVFKLMMILAMN--EKDKKKKK 237

RESULT 4
US-09-115-934A-3
; Sequence 3, Application US/09115934A
; Patent No. 6130317
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Xu, Qunli
; TITLE OF INVENTION: BAX Inhibitor Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/115,934A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/818,514
; FILING DATE: 14-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-115-934A-3

Query Match          37.5%; Score 477.5; DB 3; Length 237;
Best Local Similarity 42.2%; Pred. No. 5.2e-48;
Matches 98; Conservative 53; Mismatches 74; Indels 7; Gaps 4;

QY 19 SYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHLWNTI--GGLLTTMACGSM 76
DB 9 NFDALLKFSHTPTSTQOHLKQVYASFAALCMFYAAGAYVHVHTFTQAGLLSALGSLIM 68
QY 77 VWLLSAPPYQ--EQKRVALLMAAALFEGASIGPLIEGINFDPISIVFGAVGCVF 134
DB 69 IWLMTATPHSHETEOKKGLLAGFAFLTGIGLPALEFCIAVNPISILPTAFMGTA 128
QY 135 SAAMLARREYLYLGGLLSSGVSLFLFWLHFPAASSIFGSGMAVFKFELFGLLV 194
DB 129 TLSALYARRRYSYLFGLGILMSALL--LSSLGNVFFGSIWLFQANLVGVLMCGF 187
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QY 195 DTQETIEKAHLGDMDYVKYKHALTFTDGFAGVFRVRLIITMLKNASKEEKKKKR 246
DB 188 DTQLIIEKAHGDQDYIWHCIDFLDFTITVFRKLMMLIAMN--EKDKKKKK 237

RESULT 5
US-09-611-175-3
; Sequence 3, Application US/096111175
; Patent No. 6545128
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; Xu, Qunli
; TITLE OF INVENTION: BAX Inhibitor Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/611,175
; FILING DATE: 06-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/115,934
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/818,514
; FILING DATE: 14-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-611-175-3

Query Match 37.5%; Score 477.5; DB 4; Length 237;
Best local Similarity 42.2%; Pred. No. 5,2e-46;
Matches 98; Conservative 53; Mismatches 74; Indels 7; Gaps 4

QY 19 SYDLKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHILWNI--GGILTTWACMGSM 76
DB 9 NFDALLKFSHITSTQHLKVKVYASFALCMFVAAAGAYVHVMTFIQGLUSALGSLILM 68
QY 77 VWLLSAPPYO--EQKRVALLMAAALPEGASIGPLIELGINFDPISYFGAFVGCVF 134
DB 69 IWLMTAPHSHTETBQKLGLLAGFAFLGIGLPALEFCIAVNPSSILPTAFMGTAIMITCF 128
QY 135 SAAAMLAARREYLYLGLLSGVSLLFWLHFPASSFIFGSGMAVFKFELYGLLVFVGIVF 194
DB 129 TLGALYARRSYFLGLGILMSALSLL--LSSLGNVFFGSIWLFQANLYVGLVVMCGFVLF 187
QY 195 DTQETIEKAHLGDMDYVKYKHALTFTDGFAGVFRVRLIITMLKNASKEEKKKKR 246
DB 188 DTQLIIEKAHGDQDYIWHCIDFLDFTITVFRKLMMLIAMN--EKDKKKKK 237

RESULT 6
US-09-362-123A-2

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;	CURRENT APPLICATION NUMBER:	US/09/9996,243	
;	PRIOR FILING DATE:	2001-11-14	
;	PRIOR APPLICATION NUMBER:	60/043787	
;	PRIOR FILING DATE:	1997-06-16	
;	PRIOR APPLICATION NUMBER:	60/062250	
;	PRIOR FILING DATE:	1997-10-17	
;	PRIOR APPLICATION NUMBER:	60/065186	
;	PRIOR FILING DATE:	1997-11-12	
;	PRIOR APPLICATION NUMBER:	60/065311	
;	PRIOR FILING DATE:	1997-11-13	
;	PRIOR APPLICATION NUMBER:	60/066770	
;	PRIOR FILING DATE:	1997-11-24	
;	PRIOR APPLICATION NUMBER:	60/075945	
;	PRIOR FILING DATE:	1998-02-25	
;	PRIOR APPLICATION NUMBER:	60/078910	
;	PRIOR FILING DATE:	1998-03-20	
;	PRIOR APPLICATION NUMBER:	60/083322	
;	PRIOR FILING DATE:	1998-04-28	
;	PRIOR APPLICATION NUMBER:	60/084600	
;	PRIOR FILING DATE:	1998-05-07	
;	PRIOR APPLICATION NUMBER:	60/087106	
;	PRIOR FILING DATE:	1998-05-28	
;	PRIOR APPLICATION NUMBER:	60/087607	
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;	PRIOR APPLICATION NUMBER:	60/087759	
;	PRIOR FILING DATE:	1998-06-02	
;	PRIOR APPLICATION NUMBER:	60/087827	
;	PRIOR FILING DATE:	1998-06-03	
;	PRIOR APPLICATION NUMBER:	60/088021	
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;	PRIOR APPLICATION NUMBER:	60/088028	
;	PRIOR FILING DATE:	1998-06-04	
;	PRIOR APPLICATION NUMBER:	60/088029	
;	PRIOR FILING DATE:	1998-06-04	
;	PRIOR APPLICATION NUMBER:	60/088030	
;	PRIOR FILING DATE:	1998-06-04	
;	PRIOR APPLICATION NUMBER:	60/088033	
;	PRIOR FILING DATE:	1998-06-04	
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;	PRIOR APPLICATION NUMBER:	60/088167	
;	PRIOR FILING DATE:	1998-06-05	
;	PRIOR APPLICATION NUMBER:	60/088202	
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;	PRIOR APPLICATION NUMBER:	60/088212	
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;	PRIOR APPLICATION NUMBER:	60/088217	
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;	PRIOR APPLICATION NUMBER:	60/088655	
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;	PRIOR APPLICATION NUMBER:	60/088734	
;	PRIOR FILING DATE:	1998-06-10	
;	PRIOR APPLICATION NUMBER:	60/088738	
;	PRIOR FILING DATE:	1998-06-10	
;	PRIOR APPLICATION NUMBER:	60/088742	
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;	PRIOR APPLICATION NUMBER:	60/088810	
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;	PRIOR APPLICATION NUMBER:	60/088824	
;	PRIOR FILING DATE:	1998-06-10	
;	PRIOR APPLICATION NUMBER:	60/088826	
;	PRIOR FILING DATE:	1998-06-10	
;	PRIOR APPLICATION NUMBER:	60/088858	
;	PRIOR FILING DATE:	1998-06-11	
;	PRIOR APPLICATION NUMBER:	60/088861	
;	PRIOR FILING DATE:	1998-06-11	
;	PRIOR APPLICATION NUMBER:	60/088876	

;	PRIOR APPLICATION NUMBER:	60/090696	;	EARLIER FILING DATE:	1997-05-23	;
;	PRIOR FILING DATE:	1998-06-25	;	EARLIER APPLICATION NUMBER:	60/047,615	;
;	PRIOR APPLICATION NUMBER:	60/090862	;	EARLIER FILING DATE:	1997-05-23	;
;	PRIOR FILING DATE:	1998-06-26	;	EARLIER APPLICATION NUMBER:	60/047,597	;
;	PRIOR APPLICATION NUMBER:	60/090863	;	EARLIER FILING DATE:	1997-05-23	;
;	PRIOR FILING DATE:	1998-06-26	;	EARLIER APPLICATION NUMBER:	60/047,502	;
;	PRIOR APPLICATION NUMBER:	60/091360	;	EARLIER FILING DATE:	1997-05-23	;
;	PRIOR FILING DATE:	1998-07-01	;	EARLIER APPLICATION NUMBER:	60/047,633	;
;	PRIOR APPLICATION NUMBER:	60/091478	;	EARLIER FILING DATE:	1997-05-23	;
;	PRIOR FILING DATE:	1998-07-02	;	EARLIER APPLICATION NUMBER:	60/047,583	;
;	PRIOR APPLICATION NUMBER:	60/091544	;	EARLIER FILING DATE:	1997-05-23	;
;	PRIOR FILING DATE:	1998-07-01	;	EARLIER APPLICATION NUMBER:	60/047,617	;
;	PRIOR APPLICATION NUMBER:	60/091519	;	EARLIER FILING DATE:	1997-05-23	;
;	PRIOR FILING DATE:	1998-07-02	;	EARLIER APPLICATION NUMBER:	60/047,618	;
;	PRIOR APPLICATION NUMBER:	60/091626	;	EARLIER FILING DATE:	1997-05-23	;
;	PRIOR FILING DATE:	1998-07-02	;	EARLIER APPLICATION NUMBER:	60/047,503	;
;	PRIOR APPLICATION NUMBER:	60/091633	;	EARLIER FILING DATE:	1997-05-23	;
;	PRIOR FILING DATE:	1998-07-02	;	EARLIER APPLICATION NUMBER:	60/047,592	;
;	PRIOR APPLICATION NUMBER:	60/091978	;	EARLIER FILING DATE:	1997-05-23	;
;	PRIOR FILING DATE:	1998-07-07	;	EARLIER APPLICATION NUMBER:	60/047,581	;
;	PRIOR APPLICATION NUMBER:	60/091982	;	EARLIER FILING DATE:	1997-05-23	;
;	PRIOR FILING DATE:	1998-07-07	;	EARLIER APPLICATION NUMBER:	60/047,584	;
;	PRIOR APPLICATION NUMBER:	60/092182	;	EARLIER FILING DATE:	1997-05-23	;
;	PRIOR FILING DATE:	1998-07-09	;	EARLIER APPLICATION NUMBER:	60/047,500	;
;	Query Match	13.0%; Score 165; DB 4; Length 345;	;	EARLIER FILING DATE:	1997-05-23	;
;	Best Local Similarity	26.3%; Pred. No. 5.3e-11;	;	EARLIER APPLICATION NUMBER:	60/047,587	;
;	Matches	61; Conservative 47; Mismatches 86; Indels 38; Gaps 11;	;	EARLIER FILING DATE:	1997-05-23	;
QY	36	HLKQVYLTCCALVASAAGAYLH---ILWNI-----GGLLT---TMACMGSMWLLSAPPYQE	87	EARLIER APPLICATION NUMBER:	60/047,613	;
Db	125	HSTYMLGIGLTLALSAISRTPVLNFMNMRGSGWTIGVTFEAWGAGMLVRSIPYDQ	184	EARLIER FILING DATE:	1997-05-23	;
QY	88	Q-----KRVALLMAALFEFASIGPTELGINPEPSIVFGAFVGCVAFFGCFSAAMLAARR	144	EARLIER APPLICATION NUMBER:	60/047,582	;
Db	185	SPGPKHLAWLLHSGVM-GAVAPLILG---GPLLIRAAWTTAGIV-GCLSTVAMCAPSE	239	EARLIER FILING DATE:	1997-05-23	;
QY	145	EYLYLGGLLSSGVSLFLWLHFASSIFGGSM-----AVFKFELYGGLLVFVGXIVF	194	EARLIER APPLICATION NUMBER:	60/047,612	;
Db	240	KELNMGAPLGVGLGV----FVSSL--GSMFLPPTTVAGATLYSVAMTGGVLVLSMFLLY	293	EARLIER FILING DATE:	1997-05-23	;
QY	195	DTQEITEKHAHGDK-----DVKKALHLFTDGFAGVFRILLIMLKNASEKE	240	EARLIER APPLICATION NUMBER:	60/047,632	;
Db	294	DTQKVIKRAEVSPMYGVQKYDPINSMLSIMYDPLNIFMRVATMTLATGGRKK	345	EARLIER FILING DATE:	1997-05-23	;
;	RESULT 8		;	EARLIER APPLICATION NUMBER:	60/047,601	;
;	US-09-149-476-493		;	EARLIER FILING DATE:	1997-05-23	;
;	Sequence 493, Application US/09149476		;	EARLIER APPLICATION NUMBER:	60/043,580	;
;	Patent No. 6420526		;	EARLIER FILING DATE:	1997-04-11	;
;	GENERAL INFORMATION:		;	EARLIER APPLICATION NUMBER:	60/043,569	;
;	APPLICANT: Rosen et al.		;	EARLIER FILING DATE:	1997-04-11	;
;	TITLE OF INVENTION: 186 Human Secreted proteins		;	EARLIER APPLICATION NUMBER:	60/043,311	;
;	FILE REFERENCE: P2002P1		;	EARLIER FILING DATE:	1997-04-11	;
;	CURRENT APPLICATION NUMBER: US/09/149,476		;	EARLIER APPLICATION NUMBER:	60/043,671	;
;	EARLIER FILING DATE: 1998-09-08		;	EARLIER FILING DATE:	1997-04-11	;
;	EARLIER APPLICATION NUMBER: PCT/US98/04493		;	EARLIER APPLICATION NUMBER:	60/043,674	;
;	EARLIER FILING DATE: 1998-03-06		;	EARLIER FILING DATE:	1997-04-11	;
;	EARLIER APPLICATION NUMBER: 60/040,162		;	EARLIER APPLICATION NUMBER:	60/043,669	;
;	EARLIER FILING DATE: 1997-03-07		;	EARLIER FILING DATE:	1997-04-11	;
;	EARLIER APPLICATION NUMBER: 60/040,333		;	EARLIER APPLICATION NUMBER:	60/043,312	;
;	EARLIER FILING DATE: 1997-03-07		;	EARLIER FILING DATE:	1997-04-11	;
;	EARLIER APPLICATION NUMBER: 60/038,621		;	EARLIER FILING DATE:	1997-04-11	;
;	EARLIER FILING DATE: 1997-03-07		;	EARLIER APPLICATION NUMBER:	60/043,672	;
;	EARLIER APPLICATION NUMBER: 60/040,626		;	EARLIER FILING DATE:	1997-04-11	;
;	EARLIER FILING DATE: 1997-03-07		;	EARLIER APPLICATION NUMBER:	60/043,315	;

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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 13.0%; Score 165; DB 4; Length 346;
Best Local Similarity 26.3%; Pred. No. 5.4e-11;
Matches 61; Conservative 47; Mismatches 86; Indels 38; Gaps 11;

QY 36 HLKQVYLTLCALVASAAGYLH--ILWNI--CGLLT---TWACMGSMVWLLSAPPYQE 87
DB 125 HSTYMLAGSIGTALSAIATSTPTVLNFMNMRGSSWVTIGVTFAMVAGAGMLVRSIPYDQ 184
QY 88 Q--KRVALLMAALFEGASIGPLIEIGINFDSIVEGAFVGCACVAFGCFSAAMLARRR 144
DB 185 SPGPKHLAWLLHSGVM-GAVVAPLTILG--GPLLIRAAWYTAGIV-GGLSTVAMCAPSE 239
QY 145 EYLYLGLLLSGVSLTLFWLHFASISFGSM-----AVKFELYGLLVFVGIVTF 194
DB 240 KFLNMGAPLGVGLGV---FVSSL--GSMFLPTTVAGATLYSVAMYGGLVFSMFLY 293
QY 195 DTQEITEKAHGDW-----DYKHALTLTDFGAVFVRILIMLKNASEKE 240
DB 294 DTQVKIKRAEVSPMYGVKQKDYFNPMSLSIYMDTLNIFMRVATMLATGGRKK 345

RESULT 9
US-09-252-991A-31434
; Sequence 31434, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31434
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31434

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180 IVLAAGALLFCGFIIYDTHSDMHK--LSPEYVLAAISLYDIINLFHLL 229

Db

RESULT 11

US-08-794-216-1

; Sequence 1, Application US/08794216

; Patent No. 5843716

; GENERAL INFORMATION:

; APPLICANT: Au-Young, Janice

; APPLICANT: Coleman, Roger

; TITLE OF INVENTION: NOVEL PROLINE-RICH MEMBRANE PROTEIN

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,216
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0196 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: Consensus
US-08-794-216-1

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; CLONE: Consensus
US-08-794-216-1

Query Match      8.6%; Score 109; DB 2; Length 311;
Best Local Similarity 24.6%; pred. No. 0.00018;
Matches 49; Conservative 28; Mismatches 76; Indels 46; Gaps 9

QY  41 YLTLCCALVASACAYLHILWNIGLLITTMACMGSMWLLSAPPQEOKRVALLMAAALF 100
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  148 YLILAC-----CQPPRRFRFPNNILLTLTFAMGFMTGTISS--MYQTK---AVIAMIIT 198
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QY  101 EGASIGPLIELGINFDPISVFGAWGVGCFSAAMLARRREYLYLGGLLSSGV--- 157
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  199 AVNYSIVTI---FCFQTKVDFSTGTCFLCVLGI-----VLLVTGIVTSIVLYF 243
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QY  158 SLILFWLHFASSIFGGSNAVFKFELY--FGLLVFVGYIVFDFQETII--EKALHGMDMYVKH 213
    :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  244 QYVWVLMH-----LYAALGAICFTFLAYDTQLVLGNRKHRTISPEDYITG 288
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QY  214 ALTLETDFGAVFVRILIIM 232
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  289 ALQIYTDIIYITFVLQIM 307
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RESULT 12

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US-08-749-289-1  
 ; Sequence 1, Application US/08749289  
 ; Patent No. 5955301  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bandman, Olga  
 ; APPLICANT: Coleman, Roger  
 ; TITLE OF INVENTION: NOVEL HUMAN GLUTAMATE-BINDING  
 ; TITLE OF INVENTION: PROTEIN  
 ; NUMBER OF SEQUENCES: 3  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Inocyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/749,289  
 ; FILING DATE: Filed Herewith  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0160 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 855-0555  
 ; TELEFAX: (415) 845-4166  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 369 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: Consensus  
 ; CLONE: 386116  
 ;

US-08-749-289-1  
 Query Match 8.4%; Score 107; DB 2; Length 369;  
 Best Local Similarity 20.8%; Pred. No. 0.00039;  
 Matches 57; Conservative 41; Mismatches 90; Indels 86; Gaps 11;  
 QY 2 EGFTSFDSQSASRNWSYDSLKFNFRQISPLVQTHLKQVYLTLCCALVSAAGAYLHILW 61  
 DB 134 EGPPSYDNQDFPATNWDKKSIR-----QAFIRKVFVLTQLSVTLSTVSVFTEV 184  
 QY 50 ASAG-----AY-----LHIL-----WNIGGLTTMACGSMVWLLS 81  
 DB 185 AEVKGFBVENWTVYVSVAFFSLIVLSCCGDFRKHFNWLVSLTASLSVWGM- 243  
 QY 82 APYQEQKRVALLMAALFEGASIGPLI-ELGINFDPISVFGAFVGCVAVFCFSAAML 140  
 DB 244 ASFYNTE---AVIMAGVITTAFCFTWTFSMQTRVDFETSCMGVLLVSMVLFIFAILCIF 300  
 QY 141 ARREYLYLGLSSGVSLFWLHFHASSIFGSMVAFKFEYFGLLVFGYIVFDQETI 200  
 DB 301 IRNR-----ILBIVAS-----LGALLEFCFLAVDTQLDL 330  
 QY 201 --EKAHGLDMYVKHALTLFTDFGAVFVRILIM 232  
 DB 331 GNKQLSLSPFEEYVFAALNLYTDIINIFLYILII 364

RESULT 13  
 US-09-328-714A-6

; Sequence 6, Application US/09328714A  
 ; Patent No. 6500940  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Salk Institute for Biological Sciences  
 ; APPLICANT: Inder M. Verma  
 ; APPLICANT: Mark Schmitt  
 ; APPLICANT: Nikunj V. Somia  
 ; TITLE OF INVENTION: LIFE GUARD (LFG) POLYNUCLEOTIDES AND  
 ; TITLE OF INVENTION: POLYPEPTIDES AND METHODS OF USE THEREOF  
 ; FILE REFERENCE: SALKINS.016A  
 ; CURRENT APPLICATION NUMBER: US/09/328,714A  
 ; CURRENT FILING DATE: 1999-06-09  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 6  
 ; LENGTH: 203  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila  
 ; US-09-328-714A-6

Query Match 8.2%; Score 104; DB 4; Length 203;  
 Best Local Similarity 21.7%; Pred. No. 0.00038;  
 Matches 51; Conservative 37; Mismatches 89; Indels 58; Gaps 10;  
 QY 2 EGFTSFDSQSASRNWSYDSLKFNFRQISPLVQTHLKQVYLTLCCALVSAAGAYLHILW 61  
 DB 18 EGTXTF-----ARNMWLF-----WVALGVWLVTLSMA-----CCSVRRQTPTNFIFL- 62  
 QY 62 NIGGLTTMACGSMVWLLSAPPYQEQKRVALLMAALFEGASIG-PLIELGINFDPISV 120  
 DB 63 ---GLFTAAQ---SFLMGVSATKYAPKE---VLMVAGTAAVCLATIFALQTKYDFDTMM 113  
 QY 121 EGAFVGCVAVFCFSAAMLARRREYLYLGLSSGVSLFWLHFHASSIFGSMVAFKFE 180  
 DB 114 GGILTIACMVVFLIFGIVAFYVKGK-----IITLYAS----- 145  
 QY 181 LVFGLLVFGVIVFDQETIIEKAH---LGDMDYVKHALTLFTDFGAVFVRILIM 232  
 DB 146 --IGALLFVLIYDTQLMGSGEHKYSISPEYFAALNLYTDIINIFLYILII 198

RESULT 14  
 US-09-198-452A-1044  
 ; Sequence 1044, Application US/09198452A  
 ; Patent No. 6559294  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Griffiths, R.  
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragme  
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pr  
 ; TITLE OF INVENTION: and treatment of infection  
 ; FILE REFERENCE: 9710-003-999  
 ; CURRENT APPLICATION NUMBER: US/09/198,452A  
 ; CURRENT FILING DATE: 1998-11-24  
 ; NUMBER OF SEQ ID NOS: 6849  
 ; SEQ ID NO 1044  
 ; LENGTH: 241  
 ; TYPE: PRT  
 ; ORGANISM: Chlamydia pneumoniae  
 ; US-09-198-452A-1044

Query Match 8.0%; Score 101.5; DB 4; Length 241;  
 Best Local Similarity 23.7%; Pred. No. 0.00096;  
 Matches 52; Conservative 41; Mismatches 93; Indels 33; Gaps 11;  
 QY 20 YDSLKNFRQISPLVQTHLKQVY-----LTLCCALVSAAGAY--LHILNIGGLTT 69  
 DB 7 YD--RDYIQDSRVQGTFSRVYGMWMTAGLIVTSCVALGLYFSGLYRSLFSEW----WVWC 60  
 QY 70 MACGSMVWLLSAPPYQEQKRV-ALLMAALFEGASIGPLIEL-GINFDPISVFCGF-- 124  
 DB 61 FATLGVSPFFINSKIOTLSVSVGGVFLLYSTLEGMFFGLLPVYAAQYGGGVWAAFGSA 120  
 QY 125 ---VGCVVVFCFSAAM--LARRREYLYLGLSSGVSLFWLHFHASSIFGSMVAFKFE 179

```
Db 121 ALVFGUAAVYGFTKSKIMTFALIGLL---VTLVF---AVVSMFVSMPLIYL 174
QY 180 ELYFGLLVFVGVIVFTQEIIE-KAHLGDMYVVKHALTL 217
Db 175 ICYGLVIVFVGLTAADAQAIRRISSITIGDNNWLSYKLSL 213

RESULT 15
US-09-252-991A-27652
; Sequence 27652, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27652
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27652
```

```
Query Match 7.9%; Score 100.5; DB 4; Length 327;
Best Local Similarity 23.7%; Pred. No. 0.0019;
Matches 54; Conservative 28; Mismatches 65; Indels 81; Gaps 11;

QY 31 PLVQTHLKQVYLTCCALVASAAGAYLHLMWIGGLLT-----MACMGSM 76
Db 4 PLAQAW----HLRACRAALALTAMPLOSLNLNARILLRGISQVFLQDPRLGLACL--L 57
QY 77 VWLLSAPPYQOKRVALLMAALFEGASIGPL-----IELGINFDPISVIFGAFV 125
Db 58 AIAVGAPP-----LIAGALLGGA-LGPLLARLLHCADSIEAGLYGYNAVLIGMLL 107
QY 126 G-----CAVVGCFSAAML-----ARREYL--YLGGLLSSG---VSLLPWLH 164
Db 108 AFRFAWSPGLVSLVALGCLASVALQRLFLHGLRRRRWLPPTYTIGFVNLGWWLVLGAWLG 167
QY 165 FASSIFGGSMA-----VFKFELYFGLLVFVGIV 193
Db 168 LAPATHGGCFSCAWSGTAEALAAQIGETIFLGEPLAGLLVWLGLLL 215
```

Search completed: September 22, 2003, 15:19:35  
Job time : 45 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: September 22, 2003, 15:20:33 ; Search time 27 Seconds

(without alignments)  
1367.613 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272

Sequence: 1 MEGFTSFDSQASNRWSY.....LIIMLNASEKEKKKKRN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: .556269 seqs, 148893369 residues

Total number of hits satisfying chosen parameters: 556269

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/2/pubpaa/FCI\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubpaa/FCIUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*

17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1272	100.0	248	11	US-09-955-526-4
2	988	77.7	244	15	US-10-167-015-16
3	963.5	75.7	247	15	US-10-219-220-274
4	935	75.1	261	15	US-10-167-015-18
5	884.5	69.5	252	15	US-10-167-015-32
6	878.5	69.1	258	15	US-10-167-015-34
7	878.5	69.1	285	15	US-10-167-015-6
8	853	67.1	252	15	US-10-167-015-6
9	786.5	61.8	250	15	US-10-167-015-2
10	772.5	60.7	255	15	US-10-219-220-273
11	688.5	54.1	213	15	US-10-219-220-87
12	499.5	39.3	140	15	US-10-219-220-88
13	491.5	38.6	236	12	US-10-263-828-74
14	484.5	38.1	141	15	US-10-167-015-8
15	483.5	38.0	255	9	US-09-925-302-516

16	339	26.7	78	15	US-10-167-015-20	Sequence 20, Appli
17	301	23.7	162	12	US-10-002-631C-4	Sequence 4, Appli
18	185	13.0	345	9	US-09-745-763-68	Sequence 68, Appli
19	185	13.0	345	9	US-09-989-722-2	Sequence 2, Appli
20	185	13.0	345	9	US-09-989-723-2	Sequence 2, Appli
21	185	13.0	345	9	US-09-989-279-2	Sequence 2, Appli
22	185	13.0	345	9	US-09-989-727-2	Sequence 2, Appli
23	185	13.0	345	10	US-09-989-731-2	Sequence 2, Appli
24	185	13.0	345	10	US-09-989-732-2	Sequence 2, Appli
25	185	13.0	345	10	US-09-991-073-2	Sequence 2, Appli
26	185	13.0	345	10	US-09-990-442-2	Sequence 2, Appli
27	185	13.0	345	10	US-09-991-163-2	Sequence 2, Appli
28	185	13.0	345	10	US-09-993-604-2	Sequence 2, Appli
29	185	13.0	345	10	US-09-990-456-2	Sequence 2, Appli
30	185	13.0	345	10	US-09-989-721-2	Sequence 2, Appli
31	185	13.0	345	10	US-09-992-598-2	Sequence 2, Appli
32	185	13.0	345	10	US-09-989-293A-2	Sequence 2, Appli
33	185	13.0	345	10	US-09-989-735-2	Sequence 2, Appli
34	185	13.0	345	10	US-09-990-444-2	Sequence 2, Appli
35	185	13.0	345	10	US-09-991-181-2	Sequence 2, Appli
36	185	13.0	345	10	US-09-989-730-2	Sequence 2, Appli
37	185	13.0	345	10	US-09-990-436-2	Sequence 2, Appli
38	185	13.0	345	10	US-09-993-687-2	Sequence 2, Appli
39	185	13.0	345	11	US-09-989-734-2	Sequence 2, Appli
40	185	13.0	345	11	US-09-997-653-2	Sequence 2, Appli
41	185	13.0	345	11	US-09-993-667-2	Sequence 2, Appli
42	185	13.0	345	11	US-09-997-428-2	Sequence 2, Appli
43	185	13.0	345	11	US-09-997-666-2	Sequence 2, Appli
44	185	13.0	345	11	US-09-990-438-2	Sequence 2, Appli
45	185	13.0	345	11	US-09-990-562-2	Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
US-09-955-526-4  
; Sequence 4, Application US/09955526  
; Publication No. US20030009785A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; TITLE OF INVENTION: Plant Cytoprotective Genes and Methods  
; FILE OF INVENTION: of Using Same  
; FILE REFERENCE: P-LJ 4868  
; CURRENT APPLICATION NUMBER: US/09/955,526  
; CURRENT FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: US 09/661,014  
; PRIOR FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Lycopersicon esculentum  
US-09-955-526-4

Query Match 100.0%; Score 1272; DB 11; Length 248;  
Best Local Similarity 100.0%; Pred. No. 7.2e-129;  
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEGFTSFDSQASNRWSYDSLKNPRQISPLVQTHLKOVYLTLCALVASAAGAYLHL 60
Db	1	MEGFTSFDSQASNRWSYDSLKNPRQISPLVQTHLKOVYLTLCALVASAAGAYLHL 60
QY	61	WNIGGLTTMACGSMVWLLSAPPYQOKRVALLMAALFEGASIGPLELGTNFDPSIV 120
Db	61	WNIGGLTTMACGSMVWLLSAPPYQOKRVALLMAALFEGASIGPLELGTNFDPSIV 120
QY	121	FGAFVGCAYVFCFSAAMLRREYLYLGGLLSSGVSLLFWLHFASSIFGSGMAVFKFE 180
Db	121	FGAFVGCAYVFCFSAAMLRREYLYLGGLLSSGVSLLFWLHFASSIFGSGMAVFKFE 180
QY	181	LYPGLLVFVGIVDFDQETIEIKAHGLGMDYVVKHALFTDFTGAVFVRILLIMLNASEKE 240

```

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 274
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-219-220-274

```

# RESULT 2

```

; Sequence 16, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Glycine max
US-10-167-015-16

```

```

Query Match 77.7%; Score 988; DB 15; Length 244;
Best Local Similarity 75.5%; Pred. No. 2.8e-98;
Matches 185; Conservative 32; Mismatches 24; Indels 4; Gaps 1;

QY 4 FTSFDSQASRNRSYDLSKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHLWNI 63
DB 4 FNSFDD---SRNRWYDILKNFRQISPVQNHKLQVYTLTCLFAVAAAVGAYLHLWNI 59
QY 64 GGLLTMACGSMVWLLSAPPYQEQKRVALLMAALFEGASIGPLIEGINFDPISIVFGA 123
DB 60 GGLTIVACMGSSFWLLSTPPEERKRVTLMAASLFGSGIGPLIDIAIHDPISIFA 119
QY 124 FVCAVFGCFSAAMALARRREYLYLGLLSSGVSLLEFWLHPASSIFGGSMAVFKELYF 183
DB 120 FVGTALAFACFSGAALVARRREYLYLGLLSSGVSLLEFWLHPASSIFGGSMAVFKELYF 179
QY 184 GLLVFGVIVDQIIEKAHLGDMYVYKHALTFTDFGAVFVRLIIMLKNAEKEKK 243
DB 180 GLLVFGVIVDQIIEKAHLGDMYVYKHALTFTDFGAVFVRLIIMLKNAEKEKK 239
QY 244 KKRKN 248
DB 240 KKRKN 244

```

# RESULT 3

```

US-10-219-220-274
; Sequence 274, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; FILE REFERENCE: 11000.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290

```

```

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 274
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-219-220-274

Query Match 75.7%; Score 963.5; DB 15; Length 247;
Best Local Similarity 74.4%; Pred. No. 1.3e-95;
Matches 186; Conservative 27; Mismatches 32; Indels 5; Gaps 2;

QY 1 MEGTSPFDSQASRNRSYDLSKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHLWNI 60
DB 1 MDAFASLFQ---SGKGWSDSLKNFRQISPAVOSHLKNVYLSLCCALMASAGAYLHLWNI 57
QY 61 WNIIGLLTMACGSMVWLLSAPPYQEQKRVALLMAALFEGASIGPLIEGINFDPISIV 120
DB 58 LNIIGLLTMACGSMVWLLSAPPYQEQKRVALLMAALFEGASIGPLIEGINFDPISIV 117
QY 121 FGAIVFGCFSAAMALARRREYLYLGLLSSGVSLLEFWLHPASSIFGGSMAVFKELYF 180
DB 118 ISAFVGSALAFACFSGAAMALARRREYLYLGLLSSGVSLLEFWLHPASSIFGGSMAVFKELYF 177
QY 181 LYFGLLVFGVIVDQIIEKAHLGDMYVYKHALTFTDFGAVFVRLIIMLKNAEKEKK 240
DB 178 IYFGLLVFGVIVDQIIEKAHLGDMYVYKHALTFTDFGAVFVRLIIMLKNAEKEKK 237
QY 241 --EKKKRRN 248
DB 238 KNEKKKKRRN 247

RESULT 4
US-10-167-015-18
; Sequence 18, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Glycine max
US-10-167-015-18

Query Match 75.1%; Score 955; DB 15; Length 261;
Best Local Similarity 73.3%; Pred. No. 1.1e-94;
Matches 178; Conservative 36; Mismatches 27; Indels 2; Gaps 1;

QY 6 SFEDSQ--SASRNRSYDLSKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHLWNI 63
DB 3 TFFNSQSSSSRSRWSYDILKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHLWNI 62
QY 64 GGLLTMACGSMVWLLSAPPYQEQKRVALLMAALFEGASIGPLIEGINFDPISIVFGA 123
DB 63 GGLTIVACGSMVWLLSTPPEERKRVTLMAASLFGSGIGPLIDIAIHDPISIFA 122
QY 124 FVCAVFGCFSAAMALARRREYLYLGLLSSGVSLLEFWLHPASSIFGGSMAVFKELYF 183
DB 123 FVATSLAFACFSAAMALARRREYLYLGLLSSGVSLLEFWLHPASSIFGGSMAVFKELYF 182

```

184	QY	GLLVFVGIVFDQTQEIIEKAHLGDMDVVKHALPFTDFGAVFVRILIIIMLNASEKEPKK	243
183	Db	GLLVFVGIVFDQTQEIIEKAHLGDMDVVKHALPFTDFGAVFVRILIIIMLNASEKEPKK	242
244	QY	KKR 246	
243	Db	KKR 245	

```

RESULT 5
US-10-167-015-32
; Sequence 32, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Zea mays
US-10-167-015-32

```

[illegible]

```

RESULT 6
US-10-167-015-34
; Sequence 34, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015

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```

; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 258
; TYPE: prt
; ORGANISM: zea mays
US-10-167-015-34

```

Query Match	69.1%	Score	878.5	DB	15	Length	258
Best Local Similarity	65.8%	Pred. No.	1.9e-46				
Matches	169	Conservative	37	Mismatches	42	Indels	9
Gaps	3						
QY	1	MEGFTGFDDQSASR-----NRWSDYSLKNFRQISPLVQTHLKQVYLTCALVASAA	53				
Db	1	MDAFYSTTASSTSSAPYGGGCGWGYDSMKNFRQISPAVQTHLKLVLTCALASSAV	60				
QY	54	GAYLHLIWNLTGGLITMACGSMVWLLSAPYQOEKRVALLMAAALFEFAGASIGPLIELGI	113				
Db	61	GAYLHVWNLTGGMLITLGGCVGSIAWLFSPVPEERKRYWLLMAAALLEGASVGLIKLAV	120				
QY	114	NFDPISYFVGAFGCVAVFGFCFSAAMLARREXYLLGGLSSGVSLFLWLHFASSIFG-G	172				
Db	121	EFDPISILVAFVGTAFACFACFSCAAMVAKREYLLGGLSSGISLLWLFQFAASIFGHQ	180				
QY	173	SMAVEKPELYGGLLVFGYIVFDQETIEKAHLGDDMDYVKAHLTFLTFDGFVAVFVRIILM	232				
Db	181	STSFMEFVYTGGLLIIFUGYMYDIQEVIERAHHGDMYIKHALTFLTFDFVAVLVRIILM	240				
QY	233	LKNASEK-EFKKKRRN	248				
Db	241	LKNAADKSDKKRRRS	257				

```

RESULT 7
US-10-167-015-6
; Sequence 6, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navairo
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 285
; TYPE: PRT
; ORGANISM: zea mays
US-10-167-015-6

```

Query Match	69.1%;	Score 878.5;	DB 15;	Length 285;
Best Local Similarity	65.8%;	Pred. No. 2.2e-86;		
Matches 169;	Conservative 37;	Mismatches 42;	Indels 9;	Gaps 3;
Qy	1	MEGTTSPFDSQSR-----NRWYDSLKNFRQISPLVQTHLKQVVLTCCLVALSAA	53	
Db	1	MDAFVTTASSTSSAPYGGCGGWDYDKMFRQISPAVQTHLKVVLTCVALASSAV	60	
Qy	54	GAYLHILWNIGGLTITMACMGSMVWLISAPPYQQRKRVALLMAALPEGASIGPLIELGI	113	
Db	61	GAYLHVNNIGGMLTLMGCVGISIAWLFVPPYVERKRYMLMAALLEGASVGLPIKIAV	120	





Query Match	38.0%;	Score 483.5;	DB 9;	Length 255;
Best Local Similarity	41.1%;	Pred. No. 7e-44;		
Matches 102;	Conservative 54;	Mismatches 79;	Indels 13;	Gaps 5
QY	3	GFTSPEDSQSASRNWSDSLKNEFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHLWN	62	
Db	17	GMNIFD-----RKINFDAULKESHITPTQOHLKKVYASFALCMFVAAAGAYVHMVTH	70	
QY	63	I--GGLLITMACGSMVWLLSAPYQ--EOKRVALLMAAALPEGASIGPLIELGINFDP	118	
Db	71	FIQAGLLSGLSIILMIWLMATPHSHETQEKRLGLAGFAFLTGVLGPALEFCIAVNP	130	
QY	119	IVFGAFVGCNAVFGCFSAAMLARRRYLYLGGLLSSGVSLLEFWLHFASSIFGGSMAVEK	178	
Db	131	ILPTAFMGTAIIFCTLSALYARRRYFLFGTILMSALSLL--LSSLGNVFGSILWLPQ	189	

Search completed: September 22, 2003, 15:29:19  
Job time : 28 secs



GenCore version 5.1.6  
 Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2003, 15:17:39 ; Search time 43 seconds

(without alignments)  
 554.647 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272

Sequence: 1 MEGTSPFDQSASNRWSY.....LIIMLKNAKEKKKKRRN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 145 summaries

Database : PIR\_76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1023.5	80.5	247	T52449	Bax inhibitor-1 (i
2	479	37.7	236	S42069	TEGT protein - rat
3	472	37.1	261	E71445	hypothetical prote
4	472	37.1	262	A85197	TEGT protein homol
5	471.5	37.1	237	I38334	TEGT (testis enhan
6	170.5	13.4	219	A10628	probable membrane
7	157.5	12.4	219	D85624	probable carrier/t
8	157.5	12.4	219	F90760	probable carrier/t
9	157.5	12.4	219	S07180	probable glutamate
10	144	11.3	266	T41414	probable receptor-
11	143.5	11.3	342	T34438	hypothetical prote
12	143	11.2	297	S63281	probable membrane
13	136.5	10.7	245	A83484	integral membrane
14	130.5	10.3	238	E81729	conserved hypothet
15	128.5	10.1	238	E71467	probable transport
16	128	10.1	236	A10142	probable membrane
17	124.5	9.8	239	T48120	hypothetical prote
18	124	9.7	231	A75462	conserved hypothet
19	123.5	9.7	231	D81441	probable integral
20	122	9.6	234	B64815	ybhl protein - Esc
21	122	9.6	234	H90736	hypothetical prote
22	122	9.6	234	A85587	hypothetical prote
23	121.5	9.6	239	Q0BEG5	HWLF2 protein - hu
24	120	9.4	222	S38835	probable glutamate
25	120	9.4	422	H64489	hypothetical prote
26	114.5	9.0	220	A64141	probable glutamate
27	114	9.0	227	G81014	conserved hypothet
28	113	8.9	223	D82210	conserved hypothet
29	112.5	8.8	230	H64634	conserved hypothet

30	112	8.8	232	2	AH0954	probable membrane
31	109.5	8.6	230	2	F71879	hypothetical prote
32	109	8.6	260	2	A12905	conserved hypothet
33	109	8.6	260	2	B97681	hypothetical prote
34	108.5	8.5	236	2	H71724	hypothetical prote
35	106	8.3	659	2	AB1293	ABC transporter (p
36	104	8.2	203	2	S53708	N-methyl-D-aspart
37	103.5	8.1	670	2	AH1664	ABC transporter (p
38	101.5	8.0	225	2	AG1350	hypothetical prote
39	101.5	8.0	236	2	E97723	hypothetical prote
40	101.5	8.0	238	2	H86611	transport permease
41	101.5	8.0	238	2	A72013	transport permease
42	99.5	7.8	225	2	AB1721	hypothetical prote
43	99.5	7.8	248	2	T01080	hypothetical prote
44	99	7.8	231	2	D97248	conserved membrane
45	98.5	7.7	511	2	JC7692	oligodendrocyte tr

## ALIGNMENTS

### RESULT 1

T52449

Bax inhibitor-1 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 24-Oct-2000 #sequence\_revision 24-Oct-2000 #text\_change 03-Nov-2000

C:Accession: T52449

R:Kawai, M.; Pan, L.; Reed, J.C.; Uchimiya, H.

FEBS Lett. 464, 143-147, 1999

A:Title: Evolutionally conserved plant homologue of the Bax Inhibitor-1 (BI-1) gene c

A:Reference number: Z26078

A:Accession: T52449

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-247 <KAW>

A:Cross-references: EMBL:AB025927; PIDN:BAA89541.2

A:Experimental source: cultivar Columbia

C:Genetics:

A:Gene: AtBI-1

C:Function:

A:Description: suppresses cell death induced by Bax

C:Superfamily: human testicular protein TEGT

Query Match	80.5%;	Score 1023.5;	DB 2;	Length 247;
Best Local Similarity	77.4%;	Pred. No. 1.4e-85;		
Matches 192;	Conservative 31;	Mismatches 24;	Indels 1;	Gaps 1;
QY	1	MEGFTSPFDQSASNRWSYDSLNFRQISPLVQTHLKQVYITLCCALVASAAGAYLHL	60	
Db	1	MDAFSFFDSQPGSRS-WSYDSLNFRQISPAVQNLKRVYITLCCALVASAFAYLHVL	59	
QY	61	WNIGGLLTWACGSMVWLLSAPPYQOKRVALLMAALFEAGSTGLIELGDFDPISV	120	
Db	60	WNIGGLITIGCTIMWLLSCPPYEHQKRLSLLFVSALGESVGLIKVAIDVDPISL	119	
QY	121	FGAFVGCVAVFCFSAAMLAHRRREYLYLGLLSGVSLLELHPFASSTFGGSMVAFKFE	180	
Db	120	ITAFVGTATAFVCFSAAMLAHRRREYLYLGLLSGVSLLELHPFASSTFGGSMVAFKFE	179	
QY	181	LYFGLLVFGYIVFTDQETIEKAHLGDMYVKAHLTFTDFCAVFRILIIIMLKNAKSE	240	
Db	180	LYFGLLVFGYIVFTDQETIEKAHLGDMYVKAHLTFTDFCAVFRILIIIMLKNAKSE	239	
QY	241	EKKKKRRN 248		
Db	240	EKKKKRRN 247		

### RESULT 2

S42069

TEGT protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000



Nature 409, 529-533, 2001

A:/title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:/reference number: A85480; MUID:21074935; PMID:11206551

A:/accession: D85624

A/status: preliminary

A/molecule type: DNA

A/residues: 1-219 <STO>

A/cross-references: GB:AE0051174; NID:g12514158; PIDN:AAG55456.1; GSPDB:GN00145; UWGP:

A/experimental source: strain O157:H7, substrain EDL933

C/genetics:

A/gene: ycaA

C/superfamily: Escherichia coli ybhL protein

Query Match 12.4%; Score 157.5; DB 2; Length 219;

Best Local Similarity 26.7%; Pred. No. 5.9e-07;

Matches 64; Conservative 45; Mismatches 80; Indels 51; Gaps 11;

QY 12 SASRNRWSDLSKNFRQISPLVOTH--LKOVY--LTLCALVASAGAYLHLIWNIGGLL 67  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 6 SSSHDRSTS-----LLSTHKVLRTYFLLSLTAFSAITATASTVLMPLSPGLI 53  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

QY 68 TTMACGSMVWLSSAPPYQKRVALLMAAL--FEGASIGPIELGINFDP-SIVFGAF 124  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

Db 54 LTLVGMGLMFLYK---MANKPTGIISAFATGFLGYILGPILNTVLSAGMGDVIAAMAL 110  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

QY 125 VGCVVVFSGCSAAAMLARREYLGLGLSSGVSLLF-----WLHFASSIFGG 172  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

Db 111 GGTFALVEFCGS-AVLTTRKDMSFLGMLMAGIVVVLGMVANFIQLPALHLAIS---- 165  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

QY 173 SMAVFEELYFGLLVFGVIYVFTQTETIEKAHLGDMDYVKHAULTLDFDGAIVRILIIM 232  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

Db 166 --AVF-----LIISGAILFETSII---HGGETNIIRATVSLXSVLYNFVLSLSIL 213  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 8

F90760

probable carrier/transport protein ECs1054 [imported] - Escherichia coli (strain O157)

C/species: Escherichia coli

C/date: 18-Jul-2001 #sequence revision 18-Jul-2001 #text\_change 02-Aug-2002

C/accession: F90760

R/hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.; gasawara, N.; yasunaga, T.; kuhara, S.; shiba, T.; hattori, M.; shinagawa, H.  
DNA Res. 8, 11-22, 2001

A/title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g

A/reference number: A99629; MUID:21156231; PMID:11258796

A/accession: F90760

A/status: preliminary

A/molecule type: DNA

A/residues: 1-219 <RAY>

A/cross-references: GB:BA000007; PIDN:BAB34477.1; PID:g13360514; GSPDB:GN00154

A/experimental source: strain O157:H7, substrain RIMD 0509952

C/genetics:

A/gene: ECs1054

C/superfamily: Escherichia coli ybhL protein

Query Match 12.4%; Score 157.5; DB 2; Length 219;

Best Local Similarity 26.7%; Pred. No. 5.9e-07;

Matches 64; Conservative 45; Mismatches 80; Indels 51; Gaps 11;

QY 12 SASRNRWSDLSKNFRQISPLVOTH--LKOVY--LTLCALVASAGAYLHLIWNIGGLL 67  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

Db 6 SSSHDRSTS-----LLSTHKVLRTYFLLSLTAFSAITATASTVLMPLSPGLI 53  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

QY 68 TTMACGSMVWLSSAPPYQKRVALLMAAL--FEGASIGPIELGINFDP-SIVFGAF 124  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

Db 54 LTLVGMGLMFLYK---MANKPTGIISAFATGFLGYILGPILNTVLSAGMGDVIAAMAL 110  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

QY 125 VGCVVVFSGCSAAAMLARREYLGLGLSSGVSLLF-----WLHFASSIFGG 172  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

Db 111 GGTFALVEFCGS-AVLTTRKDMSFLGMLMAGIVVVLGMVANFIQLPALHLAIS---- 165  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

QY 173 SMAVFEELYFGLLVFGVIYVFTQTETIEKAHLGDMDYVKHAULTLDFDGAIVRILIIM 232  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

C;Accession: T41414  
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.  
submitted to the EMBL Data Library, September 1998  
A;Reference number: Z21954  
A;Accession: T41414  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-266 <WOO>  
A;Cross-references: EMBL:AL031798; PIDN:CAA21183.1; GSPDB:GNO0068; SPDB:SPCC576.04  
A;Experimental source: strain 972h-; cosmid c576  
C;Genetics:  
A;Gene: SPDB:SPCC576.04  
A;Map position: 3

Query Match 11.3%; Score 144; DB 2; Length 266;  
Best Local Similarity 24.9%; Pred. No. 1.2e-05;  
Matches 65; Conservative 39; Mismatches 95; Indels 62; Gaps 14;

QY 10 SOSASRNRSYDSLSKNEFRQISPLVQ-----THLKOVYLTLCCAL-VASAAGA--YLHI 59  
Db :|||:||::||::||::||::||::||::||::||::||::||::||::||::||  
29 NESATEN----PAVDQPKNTTPVAECSAKSTRMAFLRKRYAILTAQLFVTSDFGGIFVLHP 84  
QY 60 LWN-----IGGLLTMACGMGMWLSSAPPYEQEKRVALLMAAALEFGASIGPL 108  
Db ::::||::||::||::||::||::||::||::||::||::||::||::||  
85 AFSEFWQMHPWFILNFELSVLVFG-----LMKPYSYPNNYTFLEFLTALEGLTGSTA 139  
QY 109 IEIGINFDPSIVGFAGVCAGAVWGCFSA--AAMLARRELYIYLGLLSGV-----SLL 160  
Db ||::||::||::||::||::||::||::||::||::||::||::||::||  
140 ITF---FSARILLEAVF---ITLGVFALTAFQSKWDFSRLGGFLYVSLWSLILPTLI 193  
QY 161 FWL-----HFASSIFGGMVAFKFELYEGLLVFVGVIYVDFQEIIEKAHLGMDYVKHALT 216  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||  
194 FFEVPSTPFDMAFAG-----PGTLVFCGYILEFDYNYLHR--YSPPEEFIMSLM 241  
QY 217 LFTDFAVAVFRILLII--MLKN 235  
Db ||::||::|||:|||||:||||  
242 LYLDFINLFIRILQILGMQN 262

RESULT 11  
T34438  
hypothetical protein K11H12.8 - Caenorhabditis elegans.  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C;Accession: T34438  
R;Bradshaw, H.  
submitted to the EMBL Data Library, February 1997  
A;Description: The sequence of C. elegans cosmid K11H12.  
A;Reference number: Z21526  
A;Accession: T34438  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-342 <BRA>  
A;Cross-references: EMBL:U88168; PIDN:AAC24402.1; GSPDB:GNO0022; CESP:K11H12.8  
A;Experimental source: strain Bristol N2; clone K11H12  
C;Genetics:  
A;Gene: CESP:K11H12.8  
A;Map position: 4  
A;Introns: 45/3; 67/1; 150/3; 186/1; 262/1; 314/2

Query Match 11.3%; Score 143.5; DB 2; Length 342;  
Best Local Similarity 23.7%; Pred. No. 1.7e-05;  
Matches 53; Conservative 47; Mismatches 86; Indels 31; Gaps 8;

QY 42 LTLCALVASAAGAYLHILNIGLLTFTMACMGSMWL-L SAPPYQBRKVALIMAAL- 99  
Db ||::||::||::||::||::||::||::||::||::||::||::||::||  
126 LTVSGVAAKSRAAIMRLTAG-GGMSLPFGTMAAMIASGMLARSIDYSTVAKHLAWAH 184  
QY 100 --PEGASIGPLIELGINFDPISIVFGAVFCGVSAAAMLARRELYIYLGLLSGV 157  
Db |||||:||::||::||::||::||::||::||::||::||::||::||::||  
185 CGVLGAVFAPLCTMA--GGVLTRAAYTAGIV-GGLSATATAPSCKFLMMSGPLAMGF 240  
QY 158 SLILFWLHFAS-----SIFGSMNAVFFELVFGLLVFWGIYVDTORIEIKFA----- 203

```
Db 241 GVVFANIGAFPLPGSALGASLA--SIVVYGLILFSAFLYDQRLVKKAAENHPHSSQ 298
      ::::: : : : | | | | : | | | | : | | | | : | | | |
QY 204 -----HLGDMYVVKHALTFTDFGAVFVRILLIM 232
      : : : : : : : : : : : : : : : : : : : : : :
Db 299 LYGSDMQIRSFDPINQMSIYMDVLNIFMRUVMIM 333
      : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
S63281
probable membrane protein YNL305C - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein N0405
C:Species: Saccharomyces cerevisiae
C:Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 19-Apr-2002
A:Accession: S63281; S60395; S66127
R:Maurer, C.T.C.; Urbanus, J.H.M.; Planta, R.J.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S63266
A:Accession: S63281
A:Molecule type: DNA
A:Residues: 1-297 <MAU>
A:Cross-references: EMBL:271581; NID:g1302402; PID:e239757; PID:g1302403; MIPS:YNL305C
R:Maurer, K.C.T.; Urbanus, J.H.M.; Planta, R.J.
Yeast 11, 1303-1310, 1995
A:Title: Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV carrying a
C, and a novel putative serine/threonine protein kinase gene.
A:Reference number: S60394; MUID:96132033; PMID:8553702
A:Accession: S60395
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-297, 'D', <MAU>
A:Cross-references: EMBL:023084
R:Maurer, K.T.C.
submitted to the EMBL Data Library, March 1995
A:Reference number: S66127
A:Accession: S66127
A:Molecule type: DNA
A:Residues: 1-297 <MAU>
A:Cross-references: EMBL:U23084; NID:g1050853; PID:g1050855
C:Genetics:
A:Map position: 14L
A:Cross-references: SGD:S0005249
C:Keywords: transmembrane protein
F:86-102/Domain: transmembrane #status predicted <TM1>
F:173-189/Domain: transmembrane #status predicted <TM2>
F:212-228/Domain: transmembrane #status predicted <TM3>
F:238-254/Domain: transmembrane #status predicted <TM4>
F:271-287/Domain: transmembrane #status predicted <TM5>

Query Match 11.2%; Score 143; DB 2; Length 297;
Best Local Similarity 24.3%; Pred. No. 1.7e-05;
Matches 65; Conservative 44; Mismatches 83; Indels 76; Gaps 13;
QY 31 PLV-OTHLKQVLTCCALVASAAGY-----LHI-LWNIGLLTLMACMGS 75
      : : : : : : : : : : : : : : : : : : : : : :
Db 44 PLIQRFMKHYLSLLSCOLLASLSPCYWASVSTSLQNTFMSHIALFYICMVSLSVC--- 100
      : : : : : : : : : : : : : : : : : : : : : :
QY 76 MWVLLSAP-----PYEQKR-----VALLMAAALFEGA 103
      : : : : : : : : : : : : : : : : : : : : : :
Db 101 -IWLAVSRPEDYASVPEPLLTGSSEPAQEORPLPHVYLSYKQKTLISIFTLSEAY 159
      : : : : : : : : : : : : : : : : : : : : : :
QY 104 STGPIELIGINPDPSIVFGAVGCGFSAAMALARRREYLYLGLSSGVSLFWL 163
      : : : : : : : : : : : : : : : : : : : : : :
Db 160 CLS-LVTLA--YDKDVTLSALLITIVVGVSLTALSER-----FENVLSATSIIYWL 210
      : : : : : : : : : : : : : : : : : : : : : :
QY 164 HF-----ASSIFGSMVAFKELYFGLL---VFVGIVFTQELIEKAHLGDMY 210
      : : : : : : : : : : : : : : : : : : : : : :
Db 211 NWGLIMTGMGTLALGWNTHSSKNFLYGLWGLTAYLFDITQLIFRKYV--PDDE 268
      : : : : : : : : : : : : : : : : : : : : : :
QY 211 VKHALTFTDFGAVFVRILLIMKNASE 238
      : : : : : : : : : : : : : : : : : : : : : :
Db 269 VRCAMWLYLDIVNLFSLIRI-LANSND 295
      : : : : : : : : : : : : : : : : : : : : : :
```

```
RESULT 13
A83484
integral membrane protein [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanov
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A:Reference number: AD3252; PMID:11756688
A:Accession: AE3484
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-245 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL5304.1; PID:g1798389; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME11859
A:Map position: I
C:Superfamily: Escherichia coli ybH protein

Query Match 10.7%; Score 136.5; DB 2; Length 245;
Best Local Similarity 29.1%; Pred. No. 5.3e-05;
Matches 64; Conservative 31; Mismatches 76; Indels 49; Gaps 10;
QY 55 AYHLHLWN---IGGLTLMACMGSMVLLSAPPQE-----QKRVALLMA--AALF---- 100
      : : : : : : : : : : : : : : : : : : : : : :
Db 29 SYMLGVNMMATGLAVTGLAEGTAVLAQSNPAFQQLLPASPLRWIMLAPLAFAVFLSF 88
      : : : : : : : : : : : : : : : : : : : : : :
QY 101 --EGASIG-----PLIELGINFDPISIVFGAVGCGFSAAMALARRREYLY 148
      : : : : : : : : : : : : : : : : : : : : : :
Db 89 RIQSLSVGTAQAIPWGYYAALVGLSL-----SSIFVFTGQSVYRFEVTRASGALSLEY 144
      : : : : : : : : : : : : : : : : : : : : : :
QY 149 -----LGLLSGVSLLFWLHPAS--SIFGSMVAFKELYFGLLVFGYIVFTQEQ 198
      : : : : : : : : : : : : : : : : : : : : : :
Db 145 TTKRNLSAMGSFLMMG--LFGILLASVVNIFLGTALQFALSIVGLIFAGLTAYDTQE 201
      : : : : : : : : : : : : : : : : : : : : : :
QY 199 IIEKAHLGD-----MDYVKHALTFTDFGAVFVRILLIM 232
      : : : : : : : : : : : : : : : : : : : : : :
Db 202 IKENYEGDAADTQGRKIVMGALRYLDLFINMFLLQFM 241
      : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
E81729
conserved hypothetical protein TC0206 [imported] - Chlamydia muridarum (strain Nigg)
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Sep-2000
C:Accession: E81729
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hicke
.; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Saizbe
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A:Reference number: AB1500; MUID:20150255; PMID:10694935
A:Accession: E81729
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-238 <TEU>
A:Cross-references: GB:AE002287; GB:AE002160; NID:g1790237; PIDN:AAF39078.1; PID:g719
A:Experimental source: strain Nigg (MoPn)
C:Genetics:
A:Gene: TC0206
C:Superfamily: Escherichia coli ybH protein

Query Match 10.3%; Score 130.5; DB 2; Length 238;
Best Local Similarity 27.2%; Pred. No. 0.00018;
Matches 66; Conservative 35; Mismatches 95; Indels 47; Gaps 12;
QY 20 YDSLKNFQISPLVQTHLKQVY-----LTLCCALVASAAGY--LHILWNTGGLLTT 69
      : : : : : : : : : : : : : : : : : : : : : :
Db 4 YD--RDYTDQSRLPQTGTSRVSRYGWNWTAGLAVTALTSGLYATGAYRTLFSLW----WVWC 57
      : : : : : : : : : : : : : : : : : : : : : :
```

```
QY 70 MACMG-----SMWLLSAPPYQEKRVALLMAAALFEGASIGPLIEL-GINFDPISIVFG 122
Db 58 FATLGVSFYIAQIQKLSVPV-----MGLFLAYSVLEGMFGTMVPVYAAQFGGGVWA 112
QY 123 AFVGCNAVFCGCSAAAMLAR-----RREYLYLGLLSSGVSLFLFWLHFASIFGGSMA 175
Db 113 AFGSAVIFGLSAAYGAFTKSDTQTQIHRILMALIGLVV--ISLGF---LVVSLFTPMPL 167
QY 176 VKFELYFGLLVFVGIVFTQETIEKAHL-----GMDY---VKHALTLFTDFGAVFVRI 228
Db 168 MYLLICYLGLIIFVGLTVVDQAQSIRRVARSVGDHGLSYKLSLIMALQMYCNVIMIFWYL 227
QY 229 LII 231
Db 228 LQI 230

RESULT 15
E71467
Probable transport permease - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C:Accession: E71467
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: E71467
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-238 <ARN>
A:Cross-references: GB:AE001354; GB:AE001273; NID:g3329280; PIDN:AAC68416.1; PID:g332928
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: ycca
C:Superfamily: Escherichia coli ybhl protein

Query Match 10.1%; Score 128.5; DB 2; Length 238;
Best Local Similarity 25.9%; Pred. No. 0.00028;
Matches 63; Conservative 38; Mismatches 95; Indels 47; Gaps 12;

QY 20 YDSLKNFRQISPLVQTHLKOVY-----LTLCCALVASAAGAY--LHILWNIGLLTT 69
Db 4 YD--RDYQDSRLPGTFFSRVYGMWTAGLAVTALTSGLYATGAYRALPFMW-----WINC 57

QY 70 MACMG-----SMWLLSAPPYQEKRVALLMAAALFEGASIGPLIEL-GINFDPISIVFG 122
Db 58 FATLGVSFYIAQIQKLSVPV-----MGLFLAYSVLEGMFGTMVPVYAAQFGGGVWA 112
QY 123 AFVGCNAVFCGCSAAAMLAR-----RREYLYLGLLSSGVSLFLFWLHFASIFGGSMA 175
Db 113 AFGSAGIIFGLSAAYGAFTKNDTQTQIHRILMALVGLV--ISLAFI---VSLFTPMPL 167
QY 176 VKFELYFGLLVFVGIVFTQETIEKAHL-----GMDY---VKHALTLFTDFGAVFVRI 228
Db 168 LYLICYLGLIIFVGLTVVDQAQSIRRVARSVGDHGLSYKLSLIMALQMYCNVIMIFWYL 227
QY 229 LII 231
Db 228 LQI 230
```

Search completed: September 22, 2003, 15:18:39  
Job time : 45 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 22, 2003, 15:17:39 ; Search time 38 Seconds  
(without alignments)  
306.911 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272  
Sequence: 1 MEGTSPFDSQASRRNSWY.....LIIMLNASKPEKKKKRRN 248

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_Al:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1023.5	80.5	247	1	BIL-ARATH
2	876.5	68.9	249	1	BIL-ORYSA
3	481.5	37.9	237	1	BIL-HUMAN
4	481.5	37.9	237	1	BIL-PAROL
5	479	37.7	236	1	BIL-RAT
6	312	24.5	245	1	BIL-DROME
7	165	13.0	345	1	GHIT-HUMAN
8	157.5	12.4	219	1	YCCA-ECOLI
9	143	11.2	297	1	YN45-YEAST
10	130.5	10.3	238	1	Y206-CHLMO
11	128.5	10.1	238	1	Y819-CHLTR
12	125.5	9.9	220	1	Y402-PASMU
13	124	9.7	231	1	Y893-DEIRA
14	123.5	9.7	231	1	Y236-CAMJE
15	122	9.6	234	1	Y8HL-ECOLI
16	121.5	9.6	239	1	U021-HCMVA
17	120	9.4	222	1	Y044-PSEAE
18	120	9.4	238	1	ZPRO-MOUSE
19	120	9.4	422	1	YF21-METJA
20	114.5	9.0	220	1	YCCA-HAEIN
21	114	9.0	227	1	Y420-NEIMA
22	113	8.9	223	1	Y058-VIBCH
23	112.5	8.8	230	1	Y920-HELPU
24	111	8.7	238	1	ZPRO-HUMAN
25	109.5	8.6	230	1	Y920-HELPU
26	108.5	8.5	236	1	Y147-RICPR
27	97	7.6	545	1	HGT1-CANAL
28	95	7.5	462	1	NHAC-BACFI
29	93.5	7.4	630	1	SSA4-CAVPO
30	93	7.3	234	1	YRJE-LACIA
31	92.5	7.3	229	1	Y358-STRPY
32	91	7.2	1124	1	TRPL-DROME
33	90	7.1	1094	1	EMBA-MYCTU

## RESULT 1

ID	BIL-ARATH	STANDARD	PRT	247 AA
AC	O9LD45			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Bax inhibitor-1 (BI-1) (AtBI-1).			
GN	BI-1 OR AT5G47120 OR K14A3.7.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
EX	MEDLINE=20086676; PubMed=10618494;			
RA	Kawai M., Pan L., Reed J.C., Ochiya H.;			
RT	"Evolutionally conserved plant homologue of the Bax inhibitor-1 (BI-1)			
RT	gene capable of suppressing Bax-induced cell death in yeast.";			
RL	FEBS Lett. 464:143-147(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia; TISSUE=Leaf;			
EX	MEDLINE=2024035; PubMed=10758491;			
RA	Sanchez P., de Torres Zabala M., Grant M.;			
RT	"AtBI-1, a plant homologue of Bax inhibitor-1, suppresses Bax-induced			
RT	cell death in yeast and is rapidly upregulated during wounding and			
RT	pathogen challenge.";			
RL	Plant J. 21:393-399(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RA	Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.;			
RA	Tabata S.;			
RT	"Structural analysis of Arabidopsis thaliana chromosome 5. XI.;"			
RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: SUPPRESSOR OF APOPTOSIS.			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).			
CC	-!- SIMILARITY: BELONGS TO THE BIL FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	-----			
DR	EMBL; AB025927; BAA89541.2; -			
DR	EMBL; AF208124; AAG35727.1; -			
DR	EMBL; AB025609; BAA98107.1; -			
DR	PIR; T52449; T52449.			
DR	InterPro; IPR006213; Bax_inhbt1.			
DR	InterPro; IPR006214; UPF0005.			

Q9a2a3 caulobacter  
O47479 loligo blee  
O9cdm7 lactococcus  
O29470 archaeoglob  
Q9bbp6 lotus japon  
Q9evn4 pseudomonas  
O51489 borrelia bu  
P47562 mycoplasma  
P28008 staphylococ  
Q95919 polyterus  
P19845 pseudomonas  
P45064 haemophilus

## ALIGNMENTS

	InterPro; IPR006213; Bax_inhbtrl.
DR	InterPro; IPR006214; UPF0005.
DR	Pfam; PF01027; UPF0005; 1.
DR	PROSITE; PS01243; Bil; 1.
KW	Apoptosis; Transmembrane.
FT	TRANSMEM 39 59 POTENTIAL.
FT	TRANSMEM 65 85 POTENTIAL.
FT	TRANSMEM 93 113 POTENTIAL.
FT	TRANSMEM 119 139 POTENTIAL.
FT	TRANSMEM 151 171 POTENTIAL.
FT	TRANSMEM 213 233 POTENTIAL.
SQ	SEQUENCE 249 AA; 27114 MW; FEAE334I73FD384 CRC64;
Query Match	68.9%; Score 876.5; DB 1; Length 249;
Best Local Similarity	66.3%; Pred. No. 5.4e-64;
Matches 165; Conservative 40; Mismatches 43; Indels 1; Gaps -1A-	
QY	1 MEGTSPDQSASRNRWSYDSLKNFRQISPLVOTHLKOVITLTCALVASAGAYLHIL 60   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :       :
Db	1 MDAYSSTSSAGAARGWGYSLSNFKPQPAPVQSHLKVLVTLCVALAAASAVGAIHVA 60   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :       :
QY	61 WNIGGLITTACMGSGMWLLSAPPYQSKRVALLMAALFE GASIQPILETGINFPDSIV 120   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :       :
Db	61 LNIIGMLTMLCGVGSIAMLFSEVPVFEEKRFGLIAALLEGASVGPLIKLADEFSDSL 120   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :       :
QY	121 FGAFVGCAVFGCFSAAMLARRELYLGGILLSGVSLFLWLHFASSIFGGSMADVFXPE 180   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :       :
Db	121 VTAFIGVTAIRGCFTAIVA YKKREYL LGILLS SGLSILLWLQFAASFHGHTGSFWFF 180   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :       :
QY	181 LYFGLLVPGVIYPDTGEIEKAHLGMVMVKUALTFDFGAVFVRILIIMLNASEK - 239   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :       :
Db	181 VFYGLLIPLGYMYVDTEIIERAHHGMDYIKHALTFIDFAVLVRILVIMLNASKDKS 240   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :       :
QY	240 EEKKKKREN 248      ::l:
Db	241 EEKKRKRS 249      ::l:
RESULT 3	
Bil_HUMAN	
ID	BIL_HUMAN STANDARD; PRT; 237 AA.
AC	P55061; O14938; Q96J50;
Dt	01-OCT-1996 (Rel. 34, Created)
Dt	28-FEB-2003 (Rel. 41, Last sequence update)
Dt	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Bax inhibitor-1 (BI-1) (Testis enhanced gene transcript).
OS	Homo sapiens (Human),
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RX	NCBI_Taxid=9606;
RP	[1]
Tissue=Tetstis;	
Medline=96015061; PubMed=8530040;	
"Identification of a novel conserved human gene, TETG.";	
Genomics 28:301-304(1995).	
SEQUENCE FROM N.A.	
Cowling R.T., Birnboim H.C.;	
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.	
SEQUENCE FROM N.A.	
TISSUE=Placenta;	
Medline=22388257; Pubmed=12477932;	
A Straussner R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L., Diatchenko L., Marusina K., Farmer A., Rubin G.M., Honig L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,	



[illegible]

DB 188 DTQLIIIEKAENGDKDYVHWSVDLFLDFTIIPRKLMLVIALNDKDKXKEKK 237

## RESULT 5

BIL\_RAT  
ID BIL\_RAT STANDARD; PRT: 236 AA.  
AC P55062; Q64712;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bax inhibitor-1 (BI-1) (Testis enhanced gene transcript).  
GN TECT OR BIL  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Testis;  
RX MEDLINE=94281747; PubMed=8012111;  
RA Walter L., Dirks B., Rothermel E., Heyens M., Szpirer C., Levan G.,  
RA Guenther E.;  
RT "A novel, conserved gene of the rat that is developmentally regulated  
in the testis."  
RL Mamm. Genome 5:216-221(1994).  
CC -!- FUNCTION: SUPPRESSOR OF APOPTOSIS (BY SIMILARITY).  
CC -!- SUBUNIT: INTERACTS WITH BCL2 AND BCL-XL (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -!- TISSUE SPECIFICITY: HIGHLY ABUNDANT IN TESTIS.  
CC -!- SIMILARITY: BELONGS TO THE BIL FAMILY.  
CC  
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CC  
CC EMBL; X75855; CAA53470.1; -;  
CC EMBL; X75856; CAA53471.1; -;  
CC FIC; S42069; S42069.  
CC InterPro; IPR006213; Bax\_inhbrtl.  
CC InterPro; IPR006214; UPF0005.  
CC Pfam; PF01027; UPF0005.1.  
CC PROSITE; PS01243; BIL; 1.  
KW Apoptosis; Transmembrane.  
FT TRANSMEM 30 50  
FT TRANSMEM 53 73 POTENTIAL.  
FT TRANSMEM 88 108 POTENTIAL.  
FT TRANSMEM 112 132 POTENTIAL.  
FT TRANSMEM 139 159 POTENTIAL.  
FT TRANSMEM 166 186 POTENTIAL.  
FT TRANSMEM 206 226 POTENTIAL.  
SQ SEQUENCE 236 AA; 26358 MW; FFA412EC1DCB7537 CRC64;  
Query Match 37.7%; Score 479; DB 1; Length 236;  
Best Local Similarity 43.1%; Pred. No. 6.6e-32;  
Matches 100; Conservative 52; Mismatches 72; Indels 8; Gaps 5;  
QY 19 SYDLKKNFRQISPLVQTHKQVYTLCCALVASAAGAYHILWNI--GGLITTMACMGSM 76  
DB 9 NFDALLKFSHTPTQOHLKKVYASFCALCMFAAGAVVHVTRFIQAGLLSALCALM 68  
QY 77 VLLLSAPPYQ--EOKRVALLMAALFEGASTGLPIELGINFDPSIVFGAVGCAVVGCF 134  
DB 69 ICLMAIPSHETEQKRLGLL-AVAFLTGVLGSPALELCIAINPSILPTAFMGTAIMITCF 127  
QY 135 SAAAMLARREYLYIGLLSSVLLFWLHFASSFTGSGMAVFKFELYFGLLVFGYIVF 194  
DB 128 SLRAYARRSYLFGGLISAMS LMF--VSSGLNFIYGLFQANLYMGLLVWCGFYLF 186  
QY 195 DTQETIEIKAHGLGDMYVVKHALTLTDFGAVFVRILLIMKNASEKEKKKKR 246

DB 187 DTQLIIIEKAENGDKDYIWHICIDLEDFVTLFRKLMLIAFN--EKDKKKEKK 236

## RESULT 6

BIL\_DROME  
ID BIL\_DROME STANDARD; PRT: 245 AA.  
AC Q9VSH3;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Probable Bax inhibitor-1 (BI-1).  
GN CG7188.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Ballev R.M., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,  
RA Beeson K.Y., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,  
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.D., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster."  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkley; TISSUE=Head;  
RX MEDLINE=22426066; PubMed=12537569;  
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,  
RA George R.A., Guarin H., Kronmiller B., Pacle J.M., Park S., Wan K.H.,  
RA Rubin G.M., Celisner S.E.;  
RT "A Drosophila full-length cDNA resource."  
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).  
CC -!- FUNCTION: SUPPRESSOR OF APOPTOSIS (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -!- SIMILARITY: BELONGS TO THE BIL FAMILY.  
CC





```

RX MEDLINE-96132033; PubMed-8553702;
RA Maurer K.C.T., Urbanus J.H.M., Planta R.J.;
RT "Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV
RT carrying a ribosomal protein gene cluster, the genes encoding a
RT plasma membrane protein and a subunit of replication factor C, and a
RT novel putative serine/threonine protein kinase gene.";
RL Yeast J1303-1310(1995).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U23084; AAC49093.1; -
DR EMBL; Z71581; CAA96233.1; -
DR PIR; S63281; S63281.
DR SGD; S0005249; YNL305C.
DR InterPro; IPR006214; UPF0005.
DR Pfam; PF01027; UPF0005; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 54 74 POTENTIAL.
FT TRANSMEM 86 106 POTENTIAL.
FT TRANSMEM 147 167 POTENTIAL.
FT TRANSMEM 172 192 POTENTIAL.
FT TRANSMEM 209 229 POTENTIAL.
FT TRANSMEM 240 260 POTENTIAL.
FT TRANSMEM 271 291 POTENTIAL.
SQ SEQUENCE 297 AA; 33645 MW; 330784DA17152BB0 CRC64;

Query Match 11.2%; Score 143; DB 1; Length 297;
Best Local Similarity 24.3%; Pred. No. 0.00011;
Matches 65; Conservative 44; Mismatches 83; Indels 76; Gaps 13;
QY 31 PLV-QTHLKQVYLTCALVASAAGAY-----LHI-LWNTGGLTTWACMGS 75
DQ 44 PIIRQFMKHYSLSCOLLASLFCYWASVSTLQNFIMSHIALFCMVVSLVSC--- 100
QY 76 MVWLLSAP-----PYQOKR-----VALLMAALFECA 103
DQ 101 -IWLAVSPEDYEASVPEPLTGSSEPAQQRRLPWVLSYKOKLTLLSIFTLSEAY 159
QY 104 SIGPLIELGPNFDPISVFGAFVGCFAVFGCSAAAMLARREYLYLGILLSSGVSLFLWL 163
DQ 160 CLS-LVTLA--YDKOTVLSALLTITIVVGVSLTALSER-----FENVLSNATSIIYWL 210
QY 164 HF-----ASSIFGSMVAFKFEIYFGLL---VFVGYIVFTQEIIEKAHLGDMDY 210
DQ 211 NWGLMIMTGMGTALLFGWNTSHSSFNLYGLWGLAIFLTAYLFDITQIFRKVY--PDDE 268
QY 211 VKHALTLFTDFGAVFVRIILIMKNASE 238
DQ 269 VRCAMLYLDIVNLFSLIIRI-LANSND 295

RESULT 10
Y206_CHLMU
ID Y206_CHLMU STANDARD; PRT; 238 AA.
AC Q9PLA1.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Hypothetical protein TC0206.
GN TC0206.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / Nigg;

RX MEDLINE-20150255; PubMed-10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Otterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolony J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE BIL FAMILY.
CC -----
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CC -----
DR EMBL; AE002287; AAF39078.1; -
DR PIR; E81729; E81729.
DR TIGR; TC0206; -.
DR InterPro; IPR006214; UPF0005.
DR Pfam; PF01027; UPF0005; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 22 42 POTENTIAL.
FT TRANSMEM 49 69 POTENTIAL.
FT TRANSMEM 78 98 POTENTIAL.
FT TRANSMEM 105 125 POTENTIAL.
FT TRANSMEM 141 161 POTENTIAL.
FT TRANSMEM 166 186 POTENTIAL.
FT TRANSMEM 208 228 POTENTIAL.
SQ SEQUENCE 238 AA; 26309 MW; 4625B1D8093657E CRC64;

Query Match 10.3%; Score 130.5; DB 1; Length 238;
Best Local Similarity 27.2%; Pred. No. 0.00094;
Matches 66; Conservative 35; Mismatches 95; Indels 47; Gaps 12;
QY 20 YDSLNKFNQISPLVOTHLKQVY-----LFLCCALVASAAGAY--LHILWNIGGLTT 69
DQ 4 YD--RDYQDSRLPCTFSRVYGVWTAGLAVTALSLGIYATGAYRTFLSLW---WWWC 57
QY 70 MACMG-----SMWLLSAPPYQEQKRVALMAALFEASIGPLIEL-GINFDPISVFG 122
DQ 58 FATLGVSVFIQAQIQKLSVPAV-----MGLFLAYSVLGEMFTGTMPVYVAAQFGGIVWA 112
QY 123 AFVGCNAVVGCCFSAAMLAR-----RREYLYLGILLSSGVSLFLWLHFASIFGGSMA 175
DQ 113 AFGSAVIFGLSAAVGAFTKSDLTQTHRLMLALIGLMV--ISLGF---LVVSLFTPMPL 167
QY 176 VKFPELYGLIVFGYIVFTQEIIEKAHL-----GDMY---VKHALTLFTDFGAVFVRI 228
DQ 168 MYLLICYLGLIIFVGLTVVDAQSIRRVARSVGDHGLSVKLSLMALQMYCNVIMFWYL 227
QY 229 LII 231
DQ 228 LQI 230

RESULT 11
Y819_CHLTR
ID Y819_CHLTR STANDARD; PRT; 238 AA.
AC O84826;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Hypothetical protein CT819.
GN CT819.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
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RP SEQUENCE FROM N.A.  
 RC STRAIN=D/3/Cx;  
 RX MEDLINE=9900809; PubMed=9784136;  
 RA Stephens R.S., Kalman S., Lammell C.J., Fan J., Marathe R., Aravind L.,  
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,  
 RA Davis R.W.;  
 RT "Genome sequence of an obligate intracellular pathogen of humans:  
 RT Chlamydia trachomatis";  
 RL Science 282:754-759(1998).  
 RC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE BII FAMILY.  
 CC  
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 CC  
 CC EMBL; AE001354; AAC68416.1; -  
 DR PIR; E71467; E71467;  
 DR InterPro; IPR006214; UPF0005.  
 DR Pfam; PF01027; UPF0005; 1.  
 KW Hypothetical protein; Transmembrane; Complete proteome.  
 FT TRANSMEM 22 42 POTENTIAL.  
 FT TRANSMEM 49 69 POTENTIAL.  
 FT TRANSMEM 78 98 POTENTIAL.  
 FT TRANSMEM 105 125 POTENTIAL.  
 FT TRANSMEM 141 161 POTENTIAL.  
 FT TRANSMEM 166 186 POTENTIAL.  
 FT TRANSMEM 208 228 POTENTIAL.  
 SQ SEQUENCE 238 AA; 26264 MW; FDI01F7B3867B8E5 CRC64;

Query Match 10.1%; Score 128.5; DB 1; Length 238;  
 Best Local Similarity 25.9%; Pred. No. 0.0014; Indels 47; Gaps 12;  
 Matches 63; Conservative 38; Mismatches 95;  
 QY 20 YDSLNKRFQISPLVOTHLKQVY-----LTLCCALVASAAGY--LHLWNIGGLLT 69  
 DB 4 YD--RDYQDSRLPCTGSSRVVGMVGTAGLAVTALTSGLYATGAYRALFPWM---WIWC 57  
 QY 70 MACMG-----SMWLLSAPPYQOKRVALLMAALFGASIGPLIEL-GINFDPSIVFG 122  
 DB 58 FATLGVSFYIOAQIKLSVPVAV-----MGLFLAYSILEGMFFGLTPVYAAQFGGGVYVA 112  
 QY 123 AFVGCVVVFGCFSAAMLAR-----RREYLYLGLLSSGVSLLFLHFASSIFGGGMA 175  
 DB 113 AFGSAGIIFGLSAAVGAFTKNDLTQIHRILMLALVGLV--ISLAFLI---VSLFTPMPL 167  
 QY 176 VKFELFYGLLVFGYIVFDQTEILEKAHL-----GDMY---VKHALFTDFTDGFVAVFKI 228  
 DB 168 LYLICYLGLIIFVGLTVVDAQSIRRVARSVDGHDGLSKYKLSLIMALQYCNVIMIFWYL 227  
 QY 229 LII 231  
 DB 228 LQI 230

RESULT 12  
 Y402\_PASMU STANDARD; PRT; 220 AA.  
 AC Q9CNM5;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein PM0402.  
 GN PM0402.  
 OS Pasteurella multocida.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Pasteurella.  
 OX NCBI\_TaxID=747;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=Pm70;  
 RX MEDLINE=21145866; PubMed=11248100;  
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;  
 RA "Complete genome sequence of Pasteurella multocida Pm70.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE BII FAMILY.  
 CC  
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 CC  
 CC EMBL; AE006076; AA02486.1; -  
 DR InterPro; IPR006214; UPF0005.  
 DR Pfam; PF01027; UPF0005; 1.  
 KW Hypothetical protein; Transmembrane; Complete proteome.  
 FT TRANSMEM 25 45 POTENTIAL.  
 FT TRANSMEM 50 70 POTENTIAL.  
 FT TRANSMEM 74 94 POTENTIAL.  
 FT TRANSMEM 105 125 POTENTIAL.  
 FT TRANSMEM 135 155 POTENTIAL.  
 FT TRANSMEM 158 178 POTENTIAL.  
 FT TRANSMEM 196 216 POTENTIAL.  
 SQ SEQUENCE 220 AA; 23936 MW; 8EEC2E3PB4B5CDD5 CRC64;

Query Match 9.9%; Score 125.5; DB 1; Length 220;  
 Best Local Similarity 25.4%; Pred. No. 0.0022; Indels 19; Gaps 10;  
 Matches 53; Conservative 44; Mismatches 93;  
 QY 32 LVQTH--LKQVYLTCCALVASAAGAYLHLWNI--GGLLTMACGSMWLLSAPPYQ- 86  
 DB 14 LLNTHKVLNRYFYELGLTLAFSAVVAYISMSLNLRPCGLILMLAGFYGLLEF---TKL 69  
 QY 87 EOKRVALLMAAL--FEGASIGPLIELGINDP-SIVEGAFVG-CAVVGCFSAAMLAR 142  
 DB 70 SNSGLILSTFAFTGFLGYTLGPIINLVVYSHGAGDIVVLAGTAATAAFAC--SAYVLT 127  
 QY 143 RREYLYLGLLSSGVSLLFLHFASSIFGGMAVFKFELYGLLVFGYIVFDQTEILEK 202  
 DB 138 KDMFSLGTIFALFIVLLGLMGVAFVFFQSPMLYTAISGLFVVFSTLG-ILYETSNII-- 184  
 QY 203 AHLGDMYVKHALFTDFTDGFVAVFKI 231  
 DB 185 -HGGETNVIKATVSIKVSILNLFISLLNI 212

RESULT 13  
 Y893\_DEIRA STANDARD; PRT; 231 AA.  
 AC Q9RVX8;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein DR0893.  
 GN DR0893.  
 OS Deinococcus radiodurans.  
 OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;  
 OC Deinococcaceae; Deinococcus.  
 OX NCBI\_TaxID=1299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;  
 RX MEDLINE=20036896; PubMed=10567266;  
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,  
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,  
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,  
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,  
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,

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RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577(1999).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE BIL FAMILY.
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CC -----
DR EMBL: AE001942; AAF10471.1; -
DR PIR: A75462; A75462.
DR TIGR: DR0893; -
DR InterPro: IPR006214; UPF0005.
DR Pfam: PF01027; UPF0005; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 26 46
FT TRANSMEM 56 76
FT TRANSMEM 84 104
FT TRANSMEM 112 132
FT TRANSMEM 142 162
FT TRANSMEM 163 183
FT TRANSMEM 206 226
FT TRANSMEM 231 AA; 24447 MW; BBB7D76A6445D9C9 CRC64;
SQ SEQUENCE 231 AA; 24447 MW; BBB7D76A6445D9C9 CRC64;

Query Match 9.7%; Score 124; DB 1; Length 231;
Best Local Similarity 26.2%; Pred. No. 0.0031;
Matches 62; Conservative 41; Mismatches 94; Indels 40; Gaps 10;

QY 23 LKNEFQISPLVQTHLKQV-----YLLCCALVASAGAYL-----HILWNIGL-LTT 59
DB 2 VASQGIQIAWTOQKTDQVTEFMARTYSWMAAGLTAAGVYALTAQNEGLAMQVASLRPL 61

QY 70 MACGMSVWLLSAPPYQOKRVALLMAALFEG-ASIGPLI--ELGINFDPISVFGAFVG 126
DB 62 MLAQLALFVLS----MFAQLRSLAAGALFVGYAALTGLTSPALLFAYSRAVITAFV 117

QY 127 CAVVFGCSAAMLAARR-----RYLYIGLLSSGVSLFWLHPASSIFGSMVAFKFE 180
DB 118 SAGTEGLMSVAGFVKKLSAMGREFLF--AVYGLVWAMLV-----NLFVGSALSLSGI 169

QY 181 LYFGLLVFGVYIVFTQETIEKHAHLG-----DMDYVKHALFTDFGAVFVRILII 231
DB 170 SMIGVFLFAGLTAYDTQMLRNIALSGISGEQERASINGALALYLDFTNIFLFLNI 226

RESULT 14
Y236 CAMJE
ID Y236_CAMJE STANDARD; PRT; 231 AA.
AC Q9P1Q8.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Hypothetical protein Cj0236c.
GN Cj0236c.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCCT 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Kettle J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,

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RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE BIL FAMILY.
CC -----
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CC -----
DR EMBL: AL139074; CAB72705.1; -
DR PIR: D81441; D81441.
DR InterPro: IPR006214; UPF0005.
DR Pfam: PF01027; UPF0005; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 36 56
FT TRANSMEM 58 78
FT TRANSMEM 83 103
FT TRANSMEM 143 163
FT TRANSMEM 170 190
FT TRANSMEM 231 AA; 25487 MW; 279E67CA380336C9 CRC64;
SQ SEQUENCE 231 AA; 25487 MW; 279E67CA380336C9 CRC64;

Query Match 9.7%; Score 123.5; DB 1; Length 231;
Best Local Similarity 26.8%; Pred. No. 0.0034;
Matches 62; Conservative 38; Mismatches 100; Indels 31; Gaps 10;

QY 20 YDSLKNEFQI-SPLVQTHLKQVYLTICCALVASAGAYLHIL-----WNIGLLTTMACMG 74
DB 8 YSRKEFEENTRSSELSIFIKQYQLFAASLLAATVGAIVGIFALASFFIQSQVTEWLLFA 67

QY 75 SNWLLSAPPYQOKRVALLMAALF-----EGASIGPLI--ELGINFDPISVFGAFVGC 127
DB 68 VEIGLFA--LOWKREAPLNVLVLFGETFCGSLTLPILLISVLALPAGGIITAAQAFALT 125

QY 128 AVVFGCSAAMLAARRREYLYLGG-----LISSGVSLFWLHPASSIFGSMVAFKFEIY 182
DB 126 TVAFAGLSVFM-NTKKFTVMGKALFVLIIVIVAASLLNLFQSSIVMLAISA----- 178

QY 183 FGLLVFGVYIVFTQETIEKHAHLGDMY-VKHALTFTDFGAVFVRILIM 232
DB 179 VAAILFSFYLYDTQNIIR---GNVETPIEGAVALYLDVNLVFSLLNIL 225

RESULT 15
YBHL_ECOLI
ID YBHL_ECOLI STANDARD; PRT; 234 AA.
AC P75768;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein ybhl.
GN YBHL OR B0786 OR C0868.
OS Escherichia coli, and
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Glasner J.A., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]

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Job time : 40 secs

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RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=89052323;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura H., Nishio Y., Saito N.,
RA Sanpei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-P., Boutin A., Hackett J., Stroud D.,
RA Maynew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE BIL FAMILY.
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CC -----
DR EMBL; AE000181; AAC73873.1; -
DR EMBL; D90716; BAA35444.1; -
DR EMBL; AE016757; AAN79341.1; ALT_INIT.
DR PIR; B64815; B64815.
DR Ecogene; EG13668; ybhL.
DR InterPro; IPR006214; UPF0005.
DR Pfam; PF01027; UPF0005; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 24 44 POTENTIAL.
FT TRANSMEM 57 77 POTENTIAL.
FT TRANSMEM 80 100 POTENTIAL.
FT TRANSMEM 103 123 POTENTIAL.
FT TRANSMEM 137 157 POTENTIAL.
FT TRANSMEM 164 184 POTENTIAL.
FT TRANSMEM 207 227 POTENTIAL.
SQ SEQUENCE 234 AA; 25902 MW; 7A59105563D5DFC8 CRC64;

Query Match 9.6%; Score 122; DB 1; Length 234;
Best Local Similarity 25.5%; Pred. No. 0.0045;
Matches 59; Conservative 41; Mismatches 81; Indels 50; Gaps 11;

QY 33 VQTHLKQVY-----LTLCALVASAAGAYLHILWN-----IGLLTJMA---CMGSM 76
DB 17 LQTYNAQVIGWTVGLLTFATFVAVYAAANVAWELLFNRLVGLIITIAQLALVIVLSAM 76
QY 77 WLLSAPPYQEQKRVALLMAALFEAGSIGPLIEIGINFDPISVFCAVFGCAVFGCSA 136
DB 77 IQKLSA-----GVTTMLFMLSALTGLTSSIF---IVYTAASIASTFVVTAGMFGAMSL 128
QY 137 AAMLARR-----REVLVY---LGLLSSGVSLFLFHLFPASSIFGGSMVAFKFLYFGLLVF 188
DB 129 YGYTTKRDLSGFGNLMFLALIGIVLASLVN--FWLK-----SEALMWAVTYIGVIVF 178
QY 189 VGVIVFDQTEII---EKAHLGMDVYVKH-----ALTFTDFGAVFVRILII 231
DB 179 VGLTAYDTOKLNMGEQIDRTSDTSNLRKYSILGAULTYLDLFNLFMLRLI 229
```

Search completed: September 22, 2003, 15:20:27



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 22, 2003, 15:17:40 ; Search time 68 Seconds  
(without alignments)  
941.133 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272  
Sequence: 1 MEGTFFDQSASRNWSY.....LIIMLNASEKEKKKKRN 248

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL-23.\*

- 1: sp-archaea.\*
- 2: sp-bacteria.\*
- 3: sp-fungi.\*
- 4: sp-human.\*
- 5: sp-invertebrate.\*
- 6: sp-mammal.\*
- 7: sp-mhc.\*
- 8: sp-organelle.\*
- 9: sp-phage.\*
- 10: sp-plant.\*
- 11: sp-rodent.\*
- 12: sp-virus.\*
- 13: sp-vertebrate.\*
- 14: sp-unclassified.\*
- 15: sp-virus.\*
- 16: sp-bacteriap.\*
- 17: sp-archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1134.5	89.2	249	10 Q93XB9	Q93xb9 nicotiana t
2	1027.5	80.8	247	10 Q8LAY4	Q8lay4 arabidopsis
3	1010.5	79.4	247	10 Q93XC0	Q93xc0 brassica na
4	1002.5	78.8	246	10 Q8W196	Q8w196 brassica ol
5	883	69.4	247	10 Q93XL2	Q93xl2 hordeum vul
6	523	41.1	146	10 Q8GT54	Q8gt54 hordeum vul
7	490.5	38.6	237	11 Q9D2C7	Q9d2c7 mus musculus
8	489.5	38.5	237	11 Q8BFY4	Q8bfy4 mus musculus
9	472	37.1	262	10 Q23599	Q23599 arabidopsis
10	435.5	34.2	187	10 Q9L7B6	Q9l7b6 arabidopsis
11	293	23.0	237	5 Q8TQAL	Q8tqal plasmodium
12	238	18.7	334	5 Q81KN3	Q81kn3 plasmodium
13	192	15.1	305	5 Q9VIB2	Q9vib2 drosophila
14	192	15.1	365	5 Q8T8Z4	Q8t8z4 drosophila
15	174.5	13.7	219	16 Q8Z061	Q8zg61 salmonella
16	172	13.5	341	5 Q9V234	Q9v234 drosophila

17	171	13.4	346	4 Q8N9T5	Q8n9t5 homo sapien
18	171	13.4	346	11 Q91VC9	Q91vc9 mus musculu
19	171	13.4	347	13 Q8AVX3	Q8avx3 xenopus lae
20	170.5	13.4	219	16 Q8Z7R5	Q8ezr5 salmoneilla
21	166	13.1	219	16 Q8EEK6	Q8eek6 shewanella
22	164	12.9	99	6 Q95309	Q95309 sus scrofa
23	157.5	12.4	219	16 Q8XD81	Q8xd81 escherichia
24	150	11.8	233	16 Q8Y034	Q8y034 raistonias
25	144	11.3	266	3 Q74888	Q74888 schizosacch
26	143.5	11.3	342	5 P91373	P91373 caenorhabdi
27	141.5	11.1	237	12 Q8Q086	Q8q086 camelpox vi
28	141.5	11.1	237	12 Q8V310	Q8v310 camelpox vi
29	136.5	10.7	245	16 Q8YEL9	Q8yel9 bruceella me
30	136.5	10.7	245	16 Q8G364	Q8g364 bruceella su
31	132	10.4	319	4 Q9Y6G2	Q9y6g2 homo sapien
32	131.5	10.3	228	12 Q8QRT8	Q8qrt8 chimpanzee
33	128	10.1	236	16 Q8ZGWL	Q8zgw1 yersinia pe
34	124.5	9.8	239	10 Q9M1V9	Q9m1v9 arabidopsis
35	123	9.7	313	5 Q8ML51	Q8ml51 drosophila
36	123	9.7	316	5 Q95T37	Q95t37 drosophila
37	123	9.7	324	5 Q9V6H7	Q9v6h7 drosophila
38	122.5	9.6	219	16 Q8D225	Q8d225 wigglewort
39	122	9.6	234	16 Q8X804	Q8x804 escherichia
40	119	9.4	284	4 Q9HCL9	Q9hcl9 homo sapien
41	118.5	9.3	239	5 Q9V6H6	Q9v6h6 drosophila
42	117.5	9.2	245	16 Q92L61	Q92l61 rhizobium m
43	116	9.1	244	5 Q8T8W2	Q8t8w2 drosophila
44	113.5	8.9	229	10 Q9AGN3	Q9agn3 oryza sativ
45	113	8.9	210	12 Q72763	Q72763 cowpox viru

## ALIGNMENTS

## RESULT 1

Q93XB9 PRELIMINARY; PRT; 249 AA.  
AC Q93XB9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Bax inhibitor 1.  
GN Bt-1.  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4097;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. SR-1; TISSUE=Leaf;  
RA Bolduc N., Pitre F., Brisson L.;  
RT "Characterization of Bax inhibitor 1 from Nicotiana tabacum."  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF390556; AAK73102.1; ...  
DR InterPro; IPR001084; Crystallin.  
DR Pfam; PF01027; UPF0005; 1.  
DR PROSITE; PS00225; CRYSTALLIN\_BETAGAMMA; 1.  
SQ SEQUENCE 249 AA; 27604 MW; 776ECC35BEEFB9F8 CRC64;

Query Match 89.2%; Score 1134.5; DB 10; Length 249;  
Best Local Similarity 87.1%; Pred. No. 7.6e-91;  
Matches 217; Conservative 21; Mismatches 10; Indels 1; Gaps 1;

QY 1 MEGTFFDQSASRNWSY.....LIIMLNASEKEKKKKRN 248  
Db 1 MEGTFFDQSASRNWSY.....LIIMLNASEKEKKKKRN 248  
QY 60 LWNIGLLTTTLCVGSIVWLMATPLYEOKRIALLMAAALFKGASIGPLIELAIDFDPST 120  
Db 61 LWNIGLLTTTLCVGSIVWLMATPLYEOKRIALLMAAALFKGASIGPLIELAIDFDPST 120

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QY 120 VGFAGVCAVFGCFSAAMARREYLYLGGLLSSGVLLFWLHFASIFGSGMAVFKF 179
DB 121 VIGAFVCAVAFGCFSAAMARREYLYLGGLLSSGVLLFWLHFASIFGSGMALFKF 180
QY 180 ELYFGLLVFGYIVFDQTEIEKAHLGDMYVKKHALTFTDFGAVFVRILIMLKNASEK 239
DB 181 EYFGLLVFGYIVFDQTEIEKAHLGDMYVKKHALTFTDFGAVFVRILIMLKNAADK 240
QY 240 EKKKKRRN 248
DB 241 EKKKKRRN 249

RESULT 2
Q8LAY4 PRELIMINARY; PRT; 247 AA.
AC Q8LAY4;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Bax inhibitor-1 like.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
DR EMBL; AY087532; AAM65074.1; -.
DR InterPro; IPR006213; Bax_inhbr1.
DR InterPro; IPR001064; Crystallin.
DR PROSITE; PS01243; BII; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR Genome Biol. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
DR EMBL; AY087532; AAM65074.1; -.
DR InterPro; IPR006213; Bax_inhbr1.
DR InterPro; IPR001064; Crystallin.
DR PROSITE; PS01243; BII; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
SQ SEQUENCE 247 AA; 27455 MW; ABB31C674362F34 CRC64;

Query Match 80.8%; Score 1027.5; DB 10; Length 247;
Best Local Similarity 77.8%; Pred. No. 1.5e-81;
Matches 193; Conservative 31; Mismatches 23; Indels 1; Gaps 1;

QY 1 MEGFTSFDSQSASRNRSYSLKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHL 60
DB 1 MDAFSFDSQPGSRS-WSYDSLKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHL 59
QY 61 WNIGLLTTCMACGSMWLLSAPPYQOKRVALLMAAALFEGASGPIELGINFDPISIV 120
DB 60 WNIGLLTTCGIGTWLLSCPPYEQOKRSLIFASAVLEGASVGPLIKVAIDVDPISIL 119
QY 121 FGAIFYGCAVFGCFSAAMARREYLYLGGLLSSGVLLFWLHFASIFGSGMAVFKFE 180
DB 120 ITAFVGTATAFVCFSAAMARREYLYLGGLLSSGVLLFWLHFASIFGSGMAVFKFE 179
QY 181 LYFGLLVFGYIVFDQTEIEKAHLGDMYVKKHALTFTDFGAVFVRILIMLKNASEK 240
DB 180 LYFGLLVFGYIVFDQTEIEKAHLGDMYVKKHALTFTDFGAVFVRILIMLKNAADK 239
QY 241 EKKKKRRN 248
DB 240 EKKKKRRN 247

RESULT 3
Q93XC0 PRELIMINARY; PRT; 247 AA.
AC Q93XC0;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Bax inhibitor 1 (Bax inhibitor-like protein).
GN BI-1 OR BII.
OS Brassica napus (Rape), and
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708, 3712;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.napus; STRAIN=cv. Westar; TISSUE=Leaf;
RA Bolduc N., Brisson L.;
RT "Characterization of Bax inhibitor 1 from Brassica napus.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.oleracea;
RA Coupe S.A., Sinclair B.K., Watson L.M., Bucknell T.T., Eason J.R.;
RT "The isolation and characterization of broccoli homologs to
RT Arabidopsis PCD genes, LSD1 and BI: their role during cell death and
RT senescence.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF390555; AAK73101.1; -.
DR EMBL; AF453320; AAL50979.1; -.
DR InterPro; IPR006213; Bax_inhbr1.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR006214; UPF0005.
DR Pfam; PF01027; UPF0005; 1.
DR PROSITE; PS01243; BII; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR SEQUENCE 247 AA; 27526 MW; F5A5B5EFF64E8DB CRC64;

Query Match 79.4%; Score 1010.5; DB 10; Length 247;
Best Local Similarity 75.4%; Pred. No. 4.6e-80;
Matches 187; Conservative 35; Mismatches 25; Indels 1; Gaps 1;

QY 1 MEGFTSFDSQSASRNRSYSLKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHL 60
DB 1 MDSFSSFDSQPGSRS-WSYDSLKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHL 59
QY 61 WNIGLLTTCMACGSMWLLSAPPYQOKRVALLMAAALFEGASGPIELGINFDPISIV 120
DB 60 WNIGLLTTCGIGTWLLSCPPYEQOKRSLIFASAVLEGASVGPLIKVAIDVDPISIL 119
QY 121 FGAIFYGCAVFGCFSAAMARREYLYLGGLLSSGVLLFWLHFASIFGSGMAVFKFE 180
DB 120 ITAFVGTATAFVCFSAAMARREYLYLGGLLSSGVLLFWLHFASIFGSGMAVFKFE 179
QY 181 LYFGLLVFGYIVFDQTEIEKAHLGDMYVKKHALTFTDFGAVFVRILIMLKNASEK 240
DB 180 LYFGLLVFGYIVFDQTEIEKAHLGDMYVKKHALTFTDFGAVFVRILIMLKNAADK 239
QY 241 EKKKKRRN 248
DB 240 EKKKKRRN 247

RESULT 4
Q8W196 PRELIMINARY; PRT; 246 AA.
AC Q8W196;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Bax inhibitor-like protein.
GN BII.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Brassica.  
 OX NCBI\_TaxID=3712;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Coupe S.A., Sinclair B.K., Watson L.M., Bucknell T.T., Eason J.R.:  
 RT "The isolation and characterization of broccoli homologs to  
 RT Arabidopsis PCO genes, LSD1 and BI: their role during cell death and  
 RT senescence."  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF453321; XAL50980.1; -  
 DR InterPro: IPR006213; Bax\_inhbr1.  
 DR InterPro: IPR001064; Crystallin.  
 DR InterPro: IPR006214; UPF0005.  
 DR Pfam: PF01027; UPF0005; 1.  
 DR PROSITE: PS01243; B1; 1.  
 DR PROSITE: PS00225; CRYSTALLIN\_BETAGAMMA; 1.  
 DR PROSITE: PS00225; CRYSTALLIN\_BETAGAMMA; 1.  
 SQ SEQUENCE 246 AA; 27375 MW; EBD0A01421B2DA2E CRC64;  
 Query Match 78.8%; Score 1002.5; DB 10; Length 246;  
 Best Local Similarity 76.0%; Pred. No. 2.2e-79;  
 Matches 187; Conservative 33; Mismatches 25; Indels 1; Gaps 1;  
 QY 1 MEGSFSPDSQASRNRSYDSLKNFRQISPLVQTHLKQVYLTLCALVASAGAYLHL 60  
 DB 1 MESFSFSPDSQGRS-WSYESLKNLHQISPSQVNHKRVYLTLCALVASAGAYLHV 59  
 QY 61 WNIIGLLTTMACGSMVWLLSAPPYQEQKRVALLMAALFEGASIGLIEGIFNPDPSIV 120  
 DB 60 WNIIGLLTTIACGIMWLLSCPPYEQKRLSLLFLSVALEGSAGVGLIKVAVDFDPSIL 119  
 QY 121 FGAIVGCAVVGCFSAAMARREYLYLGLLSSGVSLFLFWLHFASSIFGGSMAVFKPE 180  
 DB 120 ITAFVGTALAFICFSAAMARREYLYLGLLSSGVSLMLWLQFASSIFGGSATFKPE 179  
 QY 181 LYEGLLVFGYIVDFQEIIEKAHLGDMYVVKHALTLFTDFGAVFVRILILMKNAEKE 240  
 DB 180 LYFGLLIFVGMVDFQEIIEKAHLGDMYVVKHALTLFTDFGAVFVRILILMKNSADKE 239  
 QY 241 EKKRR 246  
 DB 240 EKKRR 245  
 RESULT 5  
 Q93XL2 PRELIMINARY; PRT; 247 AA.  
 ID Q93XL2  
 AC Q93XL2;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE BAX inhibitor 1.  
 GN PBI-1.  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Pallas; TISSUE=Leaf;  
 RA Hueckelhoven R.; Trujillo M., Kogel K.H.;  
 RT "Expression analysis of putative cell death regulator genes in near-  
 RT isogenic, resistant and susceptible barley lines inoculated with the  
 RT powdery mildew fungus."  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ290421; CAC37797.1; -  
 DR InterPro: IPR006214; UPF0005.

DR Pfam: PF01027; UPF0005; 1.  
 SQ SEQUENCE 247 AA; 26962 MW; 4DBDEFLEFAE22CC4 CRC64;  
 Query Match 69.4%; Score 883; DB 10; Length 247;  
 Best Local Similarity 67.8%; Pred. No. 5.5e-69;  
 Matches 164; Conservative 36; Mismatches 42; Indels 0; Gaps 0;  
 QY 6 SPFDSQASRNRSYDSLKNFRQISPLVQTHLKQVYLTLCALVASAGAYLHLNIGG 65  
 DB 3 AFYSTSSRAASGCHGDSLKNFRQISPAVQSHLKLVTLCFALASSAVGAYLHIALNIGG 62  
 QY 66 LTTMACGSMVWLLSAPPYQEQKRVALLMAALFEGASIGLIEGIFNPDPSIVFGAV 125  
 DB 63 MLTMLACVGTIAWMFSPVYVEERKFRGLLGMGAALLEGASVGLIELAIDFDSILVTGFV 122  
 QY 126 GCAVVGCFSAAMARREYLYLGLLSSGVSLFLFWLHFASSIFGGSMAVFKFELYFGL 185  
 DB 123 GTAFVCGFSGAATIAKREYLYLGLLSSGVSLILWLQFVTSFGHSSGSMFVYFGL 182  
 QY 186 LVFVGIVDFQEIIEKAHLGDMYVVKHALTLFTDFGAVFVRILILMKNAEKEKKK 245  
 DB 183 LIFLGVMYVDFQEIIEKAHLGDMYVVKHALTLFTDFGAVFVRILILMKNAGDKSDKKK 242  
 QY 246 RR 247  
 DB 243 RK 244  
 RESULT 6  
 Q8GT54 PRELIMINARY; PRT; 146 AA.  
 ID Q8GT54  
 AC Q8GT54;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Putative BAX inhibitor 1 (Fragment).  
 GN PBI-1.  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Pallas; TISSUE=Primary leaf;  
 RA Hueckelhoven R.; Kogel K.H.;  
 RT "A BAX inhibitor 1 homologue is expressed differentially in barley  
 RT primary leaves under pathogen attack."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ278816; CAC82183.1; -  
 DE NON\_TER 1  
 FT NON\_TER 146  
 SQ SEQUENCE 146 AA; 15347 MW; A63D88030B7EE696 CRC64;  
 Query Match 41.1%; Score 523; DB 10; Length 146;  
 Best Local Similarity 67.1%; Pred. No. 6.3e-36;  
 Matches 98; Conservative 21; Mismatches 27; Indels 0; Gaps 0;  
 QY 10 SQSASRNRSYDSLKNFRQISPLVQTHLKQVYLTLCALVASAGAYLHLNIGGLTT 69  
 DB 1 TSSAAASGCHGDSLKNFRQISPAVQSHLKLVTLCFALASSAVGAYLHIALNIGGLTM 60  
 QY 70 MACGSMVWLLSAPPYQEQKRVALLMAALFEGASIGLIEGIFNPDPSIVFGAV 129  
 DB 61 LACVGTIAWMFSPVYVEERKFRGLLGMGAALLEGASVGLIELAIDFDSILVTGFV 120  
 QY 130 VFCGFSAAAMARREYLYLGLLSS 155  
 DB 121 AFGCFSGAATIAKREYLYLGLLSS 146  
 RESULT 7  
 Q9D2C7



[1]
SEQUENCE FROM N.A.
RX MEDLINE-98121113; PubMed=9461215;
RA Bevan M., Bancroft J., Bent E., Love K., Goodman H., Dean C.,
RA Bergkamp R., Dirkse W., van Staveren M., Stiekema W., Drost L.,
RA Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,
RA Wedler E., Wambutt R., Weitzenecker T., Pohl T.M., Terryn N.,
RA Gielen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
RA Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kottler P.,
RA Entian K.D., Rieger M., Schaeffer M., Funk B., Mueller-Auer S.,
RA Silvey M., James R., Montfort A., Pons A., Puigdomenech P., Douka A.,
RA Vouklatou E., Milioni D., Hatzipoulos P., Piravandi E., Obermaier B.,
RA Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T.,
RA Palme K., Benes V., Rechman S., Ansoerge W., Cooke R., Berger C.,
RA Delsenij M., Voet M., Volckaert G., Mewes H.W., Klosterman S.,
RA Schueller C., Chalwatzis N.;
RA "Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of
RA Arabidopsis thaliana.";
RL Nature 391:485-488(1998).
[2]
SEQUENCE FROM N.A.
RP EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBSJ databases.
DR EMBL; 297343; CAB10538.2; -
DR EMBL; AL161546; CAB78761.1; -
DR InterPro; IPR006213; Bax\_inhbr1.
DR InterPro; IPR006214; UPF0005.
DR Pfam; PF01027; UPF0005; 1.
DR PROSITE; PS01243; B11; 1.
SQ SEQUENCE 262 AA; 29337 MW; 04111B60CE90F24F CRC64;
Query Match 37.1%; Score 472; DB 10; Length 262;
Best Local Similarity 61.7%; Pred. No. 3.2e-33;
Matches 95; Conservative 22; Mismatches 37; Indels 0; Gaps 0;
QY 87 EKKRYALLMAALFAGSGTLLIEGINFDPISVFGAVGCGFSAAMLAARREY 146
DB 94 EAKRLYLFLFALLGASGVPIMIVDFDSSVLVTAFTVGTAVFCFSAAMLAARREY 153
QY 147 LYLGLSSGVSLLFWLHFAISFGSGMAVFKFLYFGLLVFGYIVFTQBIIEKAHLG 206
DB 154 LYHGASLACCSILMWVQIASSIFGSGTVYKFKLYFGLLVFGYIVFTQBIIEKAHLG 213
QY 207 DMDYVKHALTFDTGAVFVRILIMLNKASKE 240
DB 214 DMDYVQHSFTFTFDPAFLVFQVILVNLMLILEKK 247
RESULT 10
Q9L7B6 PRELIMINARY; PRT; 187 AA.
AC Q9L7B6
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Similarity to Bax inhibitor-1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI\_TaxID=3702;
[1]
SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI.";
RL Submitted (APR-1999) to the EMBL/Genbank/DBSJ databases.
DR EMBL; AB025609; BAA98108.1; -
DR InterPro; IPR006213; Bax\_inhbr1.
DR PROSITE; PS01243; B11; 1.
SQ SEQUENCE 187 AA; 20867 MW; 876978A70592CF1E CRC64;

Query Match 34.2%; Score 435.5; DB 10; Length 187;
Best Local Similarity 50.0%; Pred. No. 3.3e-30;
Matches 96; Conservative 32; Mismatches 47; Indels 17; Gaps 4;
QY 62 NTGGLLTLMACGSMV-WLLSAPPYQOEKRVALLMAALFEGASGTPIELGINFDPSTIV 120
DB 4 NITGGITITLGLVSLLEHVSCPYPYKHKIRFSLLLFGLVHGASVGPCKIKSTIDIDSSIL 63
QY 121 ECAFVGCAVFCFSAAMLAARREYLYLGLLSGVSLFWL---HFASIFGGSNAV 176
DB 64 ITAFITAVIFCFSAAMLAARREYLYLGLLSGVSLFWLKNDDOPAS-----AT 116
QY 177 EFKEFLYGLLVFGYIVFTQBIIEKAHLGMDYVKHALTFDTGAVFVRILIMLNKA 236
DB 117 VEIQMYLGLLVFGYIVFTQBIIEKAHLGMDYVAVHSLYLYIGFVRVFLQILSILMNWTS 176
QY 237 SEKEKKKKRRN 248
DB 177 AD-----RIRN 183
RESULT 11
Q8IQAL PRELIMINARY; PRT; 237 AA.
AC Q8IQAL;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE CG7188-PB.
GN CG7188.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI\_TaxID=7227;
[1]
SEQUENCE FROM N.A.
RX MEDLINE-20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Fandel M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA April J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delecher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Moberg C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RL "The genome sequence of *Drosophila melanogaster*."  
 RN Science 287:2185-2195(2000).  
 RP [2]  
 RQ SEQUENCE FROM N.A.  
 RA Celisner S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,  
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
 RA Banzon J., An H., Baldwin D., Banzon K.Y., Busam D.A.,  
 RA Carlson J.W., Center A., Champs M., Davenport L.B., Dietz S.M.,  
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
 RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,  
 RA Gonzalez M., Houch J., Hoskins R.A., Hostin D., Howland T.J.,  
 RA Ilegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
 RA McIntosh T.C., Moy M., Murphy B., Nelson K.A., Nunoo J.,  
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,  
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
 RA Stapleton M., Strong R., Svirskaas R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 RL "Sequencing of *Drosophila melanogaster* genome."  
 RP Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RQ [3]  
 RQ SEQUENCE FROM N.A.  
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,  
 RA Tupy J.L., Bergman C., Carlson J.W., Celisner S.E.,  
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,  
 RA Searle S.M.J., Smith E., Shu S., Smutnack F., Whitfield E.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 RL "Annotation of *Drosophila melanogaster* genome."  
 RP Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RQ [4]  
 RQ SEQUENCE FROM N.A.  
 RA Adams M.D., Celisner S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RP [5]  
 RQ SEQUENCE FROM N.A.  
 RA FlyBase:  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE003556; AAN12018.1; -.  
 RQ SEQUENCE 237 AA; 26468 MW; E5F54AA6DBAA84A6 CRC64;  
 Query Match 33.0%; Score 293; DB 5; Length 237;  
 Best Local Similarity 24.4%; Pred. No. 1e-17;  
 Matches 72; Conservative 44; Mismatches 81; Indels 12; Gaps 4;  
 QY 31 PLVQTHLKQVLTCCALVASAGAYLHI--LWNTGGLLTTCMACGSMVWLLSAPPYQEQ 88  
 DB 25 PYVREHLSKVYVVLGSGTAAATAMGAMQMRDFLDLG----VLAAVATLVVLGLHFYKDD 80  
 QY 89 -----KRVALLMAALFFEGASIGPLIELGINFDPISIVFGAFVGCFAVFCFSAAAMLARR 143  
 DB 81 GKNYTRIGMLYAFGFCGSGILGPLLGYICSINPAIILSALTGTFTVTSLSALLAEQ 140  
 QY 144 REYLYGLLSGVSLLFWLHPASSIFGSGMAVFKFELYGLLVGVYIVDTQBIIEKA 203  
 DB 141 GKLYLGGMLVSVINTMALLSLFNMFV-KSYEVQVQLYVGVFVMAAFIVYDTQNIKEK 199  
 QY 204 HLGDMYKVKHALTFTDFGAEVRLIIM 232  
 DB 200 RGNRDVVVOHALDLFDLFLMSFRLLIIL 228  
 RESULT 12  
 Q81KN3 PRELIMINARY; PRT; 334 AA.  
 AC Q81KN3;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 GN PF14\_0571.  
 OS Plasmodium falciparum (isolate 3D7).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=36329;  
 RP [1]  
 RQ SEQUENCE FROM N.A.  
 RC STRAIN=3D7;  
 RX MEDLINE=22255705; PubMed=12368864;  
 RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,  
 RA Carlson J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,  
 RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,  
 RA Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,  
 RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,  
 RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,  
 RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,  
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,  
 RA Fraser C.M., Barrell B.;  
 RL "Genome sequence of the human malaria parasite *Plasmodium falciparum*."  
 RT Nature 419:498-511(2002).  
 RL EMBL; AE014825; AAN37184.1; -.  
 DR Hypothetical protein.  
 KW SEQUENCE 334 AA; 39849 MW; 62E1138B99BA140D CRC64;  
 QY 4 FTSPF-----DSQASRNRSYDSLKFRQISPLV---QTHLKQVLTCCALVASAA 53  
 DB 81 FTNIFGYNIEKMDPLNQIKKQRIINLSNMFSPLENEERHLLKIYGLLGMTIVSAL 140  
 QY 54 GAYLHLW-NIGGLTTCMACGSMVWLLSA--PPYQ--EOKRVALLMAALFFEGASIGPL 108  
 DB 141 SCYVDIVYKVPREFIASIISLVCSFLLASSCNHSQLVDTSKRLVYVYFAGI--SSSIGVL 198  
 QY 109 IELGINF----DPSIVFGAFVGCFAVFCFSAAAMLARRREYLYGLLSGVSLLFWLH 164  
 DB 199 ISDYINYYVNLNPSILPLAFFGSLIFCCSLAATFSKNRISIFLGAVLCVCSYMALIS 258  
 QY 165 PASSIFGSGMAVFKFELYGLLVGVYIVDTQBIIEKAHLGDMYKVKHALTFTDFGAV 224  
 DB 259 F-MNEFFIRSKEDYTLTYTGFFMYGFLVDTQITLDFRGNKDYIMHSICLYLDLVL 317  
 QY 225 FVRILIMLKNASEKEKKKK 245  
 DB 318 FTHLLRL---GQKEKKKK 334  
 RESULT 13  
 Q9VIB2 PRELIMINARY; PRT; 305 AA.  
 AC Q9VIB2;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE CG1287 protein.  
 GN CG1287.  
 OS *Drosophila melanogaster* (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; *Drosophila*.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RQ SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champs M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis J.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lakso P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Stairs R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AE003671; AAF54013.1; -  
 DR FlyBase; FBgn0037506; CG1287.  
 SQ SEQUENCE 305 AA; 32546 MW; 0F25177F36ECA99D CRC64;

Query Match 15.1%; Score 192; DB 5; Length 305;  
 Best Local Similarity 25.7%; Pred. No. 8.1e-09;  
 Matches 61; Conservative 49; Mismatches 87; Indels 40; Gaps 8;  
 QY 36 HLKQVYTLCCALVAAGAY-----LHLNIGGLTTMACM-----GSMWLLSAPP 84  
 DB 85 HATYAFGASGVTAASAVAFQSDAMMALTRSGVWASLVTLGLVWLSGSIAQGLEVP 144  
 QY 85 YQEKRVALLMAALFEGASIGPLIEGINDPSIVFGAVGCGVFCFSAAAMLARR 144  
 DB 145 GFAGAKOLAWLVHCAVL-GAVLAPMCLLG-----GPILTKALYTSIGVGLSTVAACAPSE 199  
 QY 145 EYLVGLLSSGVSLLF-----WLHFASIFGGSMAVFKFELYFGLVFGVIVFTQ 197  
 DB 200 KFLHMGGLAIGLVGVFASSLASMLPPTTAVGAG---LASMSLYGGLLIFSGFLLYDTQ 256  
 QY 198 EIEKAHLGDM-----DYVKHALTLFTDFGAVFVRILIMLNKASEKEKKRRN 248  
 DB 257 RIVKSAELYPOYSKFPYDPINHALAIYMDALNIFIRIAILAGD-----QKRKN 305

RESULT 14  
 Q87824  
 ID Q87824 PRELIMINARY; PRT; 365 AA.  
 AC Q87824;  
 DT 01-JUN-2002 (TReMBLrel. 21, Created)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
 DE AT14090p.  
 GN CG1287.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,

RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,  
 RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celniker S.,  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY075204; AAL68072.1; -  
 DR FlyBase; FBgn0037506; CG1287.  
 SQ SEQUENCE 365 AA; 39108 MW; 676C61176F923745 CRC64;

Query Match 15.1%; Score 192; DB 5; Length 365;  
 Best Local Similarity 25.7%; Pred. No. 9.8e-09;  
 Matches 61; Conservative 49; Mismatches 87; Indels 40; Gaps 8;  
 QY 36 HLKQVYTLCCALVAAGAY-----LHLNIGGLTTMACM-----GSMWLLSAPP 84  
 DB 145 HATYAFGASGVTAASAVAFQSDAMMALTRSGVWASLVTLGLVWLSGSIAQGLEVP 204  
 QY 85 YQEKRVALLMAALFEGASIGPLIEGINDPSIVFGAVGCGVFCFSAAAMLARR 144  
 DB 205 GFAGAKOLAWLVHCAVL-GAVLAPMCLLG-----GPILTKALYTSIGVGLSTVAACAPSE 259  
 QY 145 EYLVGLLSSGVSLLF-----WLHFASIFGGSMAVFKFELYFGLVFGVIVFTQ 197  
 DB 260 KFLHMGGLAIGLVGVFASSLASMLPPTTAVGAG---LASMSLYGGLLIFSGFLLYDTQ 316  
 QY 198 EIEKAHLGDM-----DYVKHALTLFTDFGAVFVRILIMLNKASEKEKKRRN 248  
 DB 317 RIVKSAELYPOYSKFPYDPINHALAIYMDALNIFIRIAILAGD-----QKRKN 365

RESULT 15  
 Q82061  
 ID Q82061 PRELIMINARY; PRT; 219 AA.  
 AC Q82061;  
 DT 01-MAR-2002 (TReMBLrel. 20, Created)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE Putative TEGT family carrier/transport protein.  
 GN YCCA OR STM1085.  
 OS Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OX NCBI\_TaxID=602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;  
 RX MEDLINE=21534948; PubMed=11677609;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2";  
 RL Nature 413:852-856(2001).  
 DR EMBL; AE008747; AAL20018.1; -  
 DR InterPro; IPR006213; Bax\_inhbt1.  
 DR InterPro; IPR006214; UPF0005.  
 DR Pfam; PF01027; UPF0005; 1.  
 DR PROSITE; PS01243; B11; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 219 AA; 23313 MW; 9FA28BACE70B8497 CRC64;

Query Match 13.7%; Score 174.5; DB 16; Length 219;  
 Best Local Similarity 29.6%; Pred. No. 1.9e-07;  
 Matches 67; Conservative 42; Mismatches 76; Indels 41; Gaps 11;  
 QY 27 RQISPLVQTH-LKQVY--LTLCCALVASAGAYLHLNIGGLTTMACMGSWLLISA 82  
 DB 9 RDRSLLSTHKVLRNTYFLLSLTALSAITASTAVLMLPSFGLLTLVGMFL--- 65  
 QY 83 PPQY-EQKRVALLMAAL--FEGASIGPLIEGINDPSIVFG-AFVCGAVVFCFSAAA 138

Db 66 -TYKTANKPVGILSAPAFITGLIIPILIMAYLSAGMDVIGLALGTALVFFCCS-AY 123  
QY 139 MLARREPLYIGLISGVSLF-----WLHFASSIFGSSMAVFKFELYFGL 186  
Db 124 VLTTRKDMSPFGMLAGIYVVLIGVANIFLOPALHLAIS-----AVF-----IL 170  
QY 187 VFVGYIVFDQOELIEKAHLGMDMDYKHAJLFTFDGAVFVRIILIM 232  
Db 171 ISSGAILYETSNI---HGGETNYIRATVSLYVSLYNIFFVSLSL 213

Search completed: September 22, 2003, 15:21:52  
Job time : 74 secs



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 22, 2003, 15:23:18 ; Search time 2813 Seconds  
(without alignments)  
3606.679 Million cell updates/sec

Title: US-09-955-526-4  
Perfect score: 1272  
Sequence: 1 MEGFTSPFDQSASRRMSY.....LIIMLNKASEKEKKKKRRN 248

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Zgapop 6.0 , Zgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2888711 segs, 2045481386 residues  
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/cgn2.1/USPTO.spool/US09955526/unat.22092003.151754.12365/app\_query.fasta.1.391  
-DB=GenEmbl -GPMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCTL=0 -LOOPEXT=0  
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-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTPM=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09955526.cgn.1.1.5265.@unat.22092003.151754.12365 -NCPU=6 -ICPU=3  
-NO.MMAP -IARGOUDRY -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
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-YGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl :  
1: gb.ba :  
2: gb.htg :  
3: gb.in :  
4: gb.om :  
5: gb.ov :  
6: gb.pat :  
7: gb.ph :  
8: gb.pl :  
9: gb.pr :  
10: gb.ro :  
11: gb.sts :  
12: gb.sy :  
13: gb.un :  
14: gb.vi :  
15: em.ba :  
16: em.fun :  
17: em.hum :  
18: em.in :  
19: em.mu :  
20: em.om :  
21: em.or :  
22: em.ov :  
23: em.pat :  
24: em.ph :  
25: em.pl :  
26: em.ro :  
27: em.sts :  
28: em.un :

29: em.vi :  
30: em.htg\_hum :  
31: em.htg\_inv :  
32: em.htg\_other :  
33: em.htg\_mus :  
34: em.htg\_pln :  
35: em.htg\_rnd :  
36: em.htg\_mam :  
37: em.htg\_vrt :  
38: em\_sy :  
39: em\_htgo\_hum :  
40: em\_htgo\_mus :  
41: em\_htgo\_other :  
  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1134.5	89.2	1293	8 AF390556	AF390556 Nicotiana
2	1027.5	80.8	1066	8 AY087532	AY087532 Arabidops
3	1023.5	80.5	775	8 AY114059	AY114059 Arabidops
4	1023.5	80.5	994	8 AY091134	AY091134 Arabidops
5	1023.5	80.5	1006	8 AF208124	AF208124 Arabidops
6	1023.5	80.5	1117	8 AB025927	AB025927 Arabidops
7	1010.5	79.4	1010	8 AF390555	AF390555 Brassica
8	1010.5	79.4	1013	8 AF453320	AF453320 Brassica
9	1002.5	78.8	1019	8 AF453321	AF453321 Brassica
10	883	69.4	744	8 HYU290421	HYU290421 Hordeum v
11	876.5	68.9	750	6 AX660456	AX660456 Sequence
12	876.5	68.9	1181	8 AB025926	AB025926 Oryza sat
13	811	63.8	1137	6 AX660801	AX660801 Sequence
14	810	63.7	1137	6 AX660802	AX660802 Sequence
15	786.5	61.8	750	6 AX660870	AX660870 Sequence
16	767	60.3	34498	8 AB025609	AB025609 Arabidops
17	688.5	54.1	484	6 AR231128	AR231128 Sequence
18	523	41.1	438	6 HYU278816	HYU278816 Hordeum v
19	512	40.3	198788	8 ATCHRV46	AL161546 Arabidops
20	512	40.3	207674	8 ATFC48	Z97343 Arabidopsis
21	499.5	39.3	527	6 AR231129	AR231129 Sequence
22	492.5	38.7	2331	10 BC005588	BC005588 Mus muscu
23	483.5	38.0	892	9 AF033095	AF033095 Homo sapi
24	483.5	38.0	2609	9 BC000916	BC000916 Homo sapi
25	483.5	38.0	2695	9 BC036203	BC036203 Homo sapi
26	482.5	37.9	1745	5 AF220548	AF220548 Paraliich
27	481	37.8	940	10 RNTBGT2	AF220548 Paraliich
28	479.5	37.7	2634	6 AR058920	AR058920 Sequence
29	479.5	37.7	2634	6 AR058921	AR058921 Sequence
30	479.5	37.7	2634	6 AR112791	AR112791 Sequence
31	479.5	37.7	2634	6 AR112792	AR112792 Sequence
32	479.5	37.7	2634	6 AR305046	AR305046 Sequence
33	479.5	37.7	2634	6 AR305047	AR305047 Sequence
34	479	37.7	896	10 RNTBGT3	AR305047 Sequence
35	473.5	37.2	2600	9 HSTBGT	AR305047 Sequence
36	470	36.9	418	11 G73645	X75856 R.norvegicu
37	468	36.8	127507	2 AP005311	X75861 H.sapiens T
38	468	36.8	155492	2 AP005304	G73645 R2957F etio
39	464.5	36.5	3339	5 BC047131	AP005304 Oryza sat
40	340	26.7	360	11 G71526	BC047131 Xenopus l
41	312	24.5	1102	3 AY058377	G71526 A61521534FM
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44	269	21.1	110032	3 AC014916	BD027963 Sequence
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					AC010040 Drosophil

RESULT 1

ALIGNMENTS

AF390556  
LOCUS AF390556 1293 bp mRNA linear PLN 28-JAN-2003  
DEFINITION Nicotiana tabacum Bax inhibitor 1 (BI-1) mRNA, complete cds.  
ACCESSION AF390556  
VERSION AF390556.1 GI:14719275  
KEYWORDS  
SOURCE  
ORGANISM Nicotiana tabacum (common tobacco)  
Nicotiana tabacum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; Lamiales; Solanales; Solanaceae; Nicotiana.  
REFERENCE  
AUTHORS 1 (bases 1 to 1293)  
TITLE Bolduc, N., Ouellet, M., Pitre, F. and Brisson, L. F.  
Molecular characterization of two plant BI-1 homologues which  
suppress Bax-induced apoptosis in human 293 cells  
JOURNAL Planta 216 (3), 377-386 (2003)  
MEDLINE 22408492  
PUBMED 12520328  
REFERENCE 2 (bases 1 to 1293)  
AUTHORS Bolduc, N., Pitre, F. and Brisson, L.  
TITLE Direct Submission  
JOURNAL Submitted (11-JUN-2001) Biochemistry and Microbiology, Laval  
University, Quebec G1K 7P4, Canada  
FEATURES  
Source Location/Qualifiers  
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BASE COUNT 296 a 243 c 304 g 450 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 8.9e-106 Length: 1293  
Score: 1134.50 Matches: 217  
Percent Similarity: 95.58% Conservative: 21  
Best Local Similarity: 87.15% Mismatches: 10  
Query Match: 89.19% Indels: 1  
DB: 8 Gaps: 1  
US-09-955-526-4 (1-248) x AF390556 (1-1293)

DB 374 ATGGCGACACCTCGTATGAAGACAAAGATACACTTCATGATGGACGTGCACTG 433  
QY 100 PheGluLysAlaSerIleGlyProLeuIleGluLeuLysIleAsnProSerIle 119  
DB 434 TTTAAAGACATCTATTGGTCCATGTAATGACTTATGACTTGGACCCAGCATTT 493  
QY 120 ValPheGlyAlaPheValGlyCysAlaValPheGlyCysPheSerAlaAlaIleMet 139  
DB 494 GTATCGGTGCTTTGTTGGTGTGCTGCTGCTTTGGTCTTCTCAGCTGGCCATG 553  
QY 140 LeuAlaArgArgArgGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 159  
DB 554 GTGCAAGCGGCAAGAGACTTATCTATGAGAGCTCTTTCATCTGCTCTCTATC 613  
QY 160 LeuPhePheLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPhe 179  
DB 614 CTTTCTGGTGTGCACTTCGCTCCATTTTGTGTGTCTATGCTGTGCTGTCAAGTTC 673  
QY 180 GluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGluIle 199  
DB 674 GAGTATTATTTTGGGCTGCTGCTGCTGCTGCTGCTATATTCATTTTGAACCCAGATATA 733  
QY 200 IleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThr 219  
DB 734 ATTGAAGAGCGACACCTGGGATTTGGACTACGATGCAAGCATGCTCGACCTCTTACA 793  
QY 220 AspPheGlyAlaValPheValArgIleLeuIleIleMetLeuLysAsnAlaSerGluLys 239  
DB 794 GATTTGTGCTGCTGTTTGTGCGCAATATATATCATATGCTGAGATGATGATCGACAG 853  
QY 240 GluGluLysLysLysLysLysArgArgAsn 248  
DB 854 GAAGAGAAAGAAAGAGAGAGAGAGAAAC 880  
RESULT 2  
LOCUS AY087532 1066 bp mRNA linear PLN 14-APR-2003  
DEFINITION Arabidopsis thaliana clone 36400 mRNA, complete sequence.  
ACCESSION AY087532  
VERSION AY087532.1 GI:21406269  
KEYWORDS  
SOURCE Full cDNA.  
ORGANISM Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
REFERENCE  
AUTHORS Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N.,  
Feidmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.  
Full-length messenger RNA sequences greatly improve genome  
annotation  
JOURNAL Genome Biol. 3 (6), RESEARCH0029 (2002)  
MEDLINE 22088475  
PUBMED 12093376  
REFERENCE 2 (bases 1 to 1066)  
AUTHORS Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and  
Feidmann, K.  
TITLE Full-length cDNA from Arabidopsis thaliana  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 1066)  
AUTHORS Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and  
Feidmann, K.  
TITLE Direct Submission  
JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,  
Malibu, CA 90265, USA  
COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made  
available to fRGC and Genbank. The following quality assessment of  
this set was done by comparison with known proteins: two percent of  
the clones are estimated to be 5'-truncated; less than one percent  
are 3'-truncated; approximately two percent represent alternative  
splice variants, including unspliced introns and spliced exons; one  
percent may contain premature stop codons; five percent may have











REFERENCE  
AUTHORS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

## TITLE

Coupe, S.A., Sinclair, B.K., Watson, L.M., Bucknell, T.T. and Eason, J.R.  
The isolation and characterization of broccoli homologs to Arabidopsis PCD genes, LSD1 and BI: their role during cell death and senescence

JOURNAL  
REFERENCE  
AUTHORS

2 (bases 1 to 1013)  
Coupe, S.A., Sinclair, B.K., Watson, L.M., Bucknell, T.T. and Eason, J.R.

## TITLE

Direct Submission  
Submitted (29-NOV-2001) Crop and Food Research, Private Bag 11 600, Palmerston North 5301, New Zealand

## FEATURES

Location/Qualifiers

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15..758

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BASE COUNT  
ORIGIN

254 a 200 c 233 g 326 t

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Pred. No.: 2.61e-93 Length: 1013  
Score: 1010.50 Matches: 187  
Percent Similarity: 89.52% Conservative: 35  
Best Local Similarity: 75.40% Mismatches: 25  
Query Match: 79.44% Indels: 1  
DB: 8 Gaps: 1

US-09-955-526-4 (1-248) x AF453320 (1-1013)

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Db 15 ATGGATTCAATCTCGCTCTTCTCGATTCTCAACCTGGTACGAGAAC--TGGACTAT 71  
QY 21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40  
Db 72 GATTCCTCAAAAACCTCGCTGAGATTCTCCCTCGTCACAGATCATCTCAAGAGGTT 131  
QY 41 TyrLeuThrLeuGlyCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60  
Db 132 TATCTCACTCTGTGTGTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 191  
QY 61 TrpAsnIleGlyLeuLeuThrTrpMetAlaCysMetGlySerMetValTrpLeuLeu 80  
Db 192 TGGAAATAGGTTGTTCTCTCACTACATTTGGATGCTTTGGAGCATGATTGGCTGCTC 251  
QY 81 SerAlaProTyrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100  
Db 252 TCTGTGCTCTCTATGACAAACAAGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 311  
QY 101 GluGlyAlaSerIleGlyProLeuIleGlnLeuGlyIleAsnHisProSerIleVal 120  
Db 312 GAAGGCTTCAAGTTGCT 371

QY 121 PheGlyAlaPheValGlyCysAlaValPheGlyCysPheSerAlaAlaMetLeu 140

Db 372 ATCACTGCGTTTGGAGACCTGATGACCTTATCTGTTCTCAAGGAGGATCTTG 431

QY 141 AlaArgArgArgGlyTyrLeuTyrLeuGlyGlyLeuLeuSerGlyValSerLeuLeu 160

Db 432 GCAGAGCGACAGAGTACCTCTACCTCGAGAGCTGTTTCATCTGCTGCTCATCTT 491

QY 161 PheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGlu 180

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QY 181 LeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnIleLeu 200

Db 552 CTCTACTTTGACCTCTGATCTTTGTGGATACATGCTGTGGACCTCAAGATTAATA 611

QY 201 GluLysAlaHisLeuGlyLysPheMetAspTyrValLysHisAlaLeuThrLeuPheThrAsp 220

Db 612 GAGAAAGCCACCTCGTGCATGATGATGATGATGATGATGATGATGATGATGATGAT 671

QY 221 PheGlyAlaValPheValArgIleLeuIleIleMetLeuLysAsnAlaSerGluGlu 240

Db 672 TTGTAGCTGT 731

QY 241 GluLysLysLysLysArgArgAsn 248

Db 732 GATAAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 755

RESULT 9 AF453321 1019 bp mRNA linear PLN 27-DEC-2001

AF453321 AF453321 Brassica oleracea bax inhibitor-like protein (BI2) mRNA, complete

DEFINITION AF453321.1 GI:17981375

ACCESSION AF453321

VERSION AF453321.1

KEYWORDS

SOURCE

ORGANISM

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 1019)

Coupe, S.A., Sinclair, B.K., Watson, L.M., Bucknell, T.T. and

Eason, J.R.

The isolation and characterization of broccoli homologs to

Arabidopsis PCD genes, LSD1 and BI: their role during cell death

and senescence

Unpublished

2 (bases 1 to 1019)

Coupe, S.A., Sinclair, B.K., Watson, L.M., Bucknell, T.T. and

Eason, J.R.

Direct Submission

Submitted (29-NOV-2001) Crop and Food Research, Private Bag 11 600,

Palmerston North 5301, New Zealand

Location/Qualifiers

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Score:	1002.50	Matches:	187	
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QY	21 AspSerLeuLysAsnPheArgGlnIleLeSerProLeuValGlnThrHisLeuLysGlnVal 40			
Db	111 GAATCTCTCAAGAACCCTCCATCAGATCTCCCGCCGCTACAGAGATCATTCACAGCGGCTT 170			
QY	41 TyrIleuThrLeuLysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60			
Db	171 TATCTCACTTATCTGTGCTTCGCTTCGCTTCCTTGGAGGCTTACCTCCAGCTCTC 230			
QY	61 TrpAsnIleGlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValIrrPheLeu 80			
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QY	81 SerAlaProPtyrGlnGlnGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100			
Db	291 TCATGTCCTCTCTTATGAGCAACAAAGAGGCTCTCATCTCTCTCTCTCTCTCTCTCTCT 350			
QY	101 GlnGlyAlaSerIleGlyProLeuIleGlnLeuGlyIleAsnPheAspProSerIleVal 120			
Db	351 GAAAGTGCTGTGTGGCCCTTATCTCAAAAGTGCCTGTGATTTGACCCAGACATCCTT 410			
QY	121 PheGlyAlaPheValIleGlyCysAlaValAlaPheGlyCysPheSerAlaAlaIleMetLeu 140			
Db	411 ATCATCGGTGTTCGGAACATGCATATAGCGTTTATCTGTTTCTCAGAGACGATGTG 470			
QY	141 AlaArgArgArgGlnTyrLeuTyrLeuGlyAlaLeuLeuSerSerGlyValSerLeuLeu 160			
Db	471 GCCAGACGCAAGAGGTATCTCTACCTCGGAGGACCTTCTCTCTCTCTCTCTCTCTCT 530			
QY	161 PheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValAlaPheLysPheGln 180			
Db	531 ATGTGGCTTACGTTTGTCTCTTCATCTCTTGTTGGTCTCGCTCCATCTTAACTTTGAG 590			
QY	181 LeuTyrPheGlyLeuLeuValPheValIleTyrIleValPheAspThrGlnIleIle 200			
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QY	201 GlnLysAlaHisLeuGlyAspMetAspTyrValIleHisAlaLeuThrLeuPheThrAsp 220			
Db	651 GAGAAAGACACACCTTAAGGGAGATATGACATATGTGAACATGATTAACCTTTTACCGCAT 710			
QY	221 PheGlyAlaValPheValArgIleLeuIleIleMetLeuLysAsnAlaSerGlnLysGln 240			
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QY	241 GlnLysLysLysLysArg 246			
Db	771 GAGGAAGAAAGAGAGAGA 788			
RESULT 10				
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DEFINITION	Hordem valigare mRNA for BAX inhibitor 1 (pBI-1 gene).			
ACCESSION	AJ290421	1	GI:13940164	
VERSION	BAJ290421.1	GI:13940164		
KEYWORDS	BAX inhibitor 1; pBI-1 gene.			

[illegible]

QY	106	GLYPROLEUINLEUIGLYLLEASNPHENSPROSERILLEVALPHEGLYALAPHEVAL	125
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QY	126	GLYCYSALAVALAPHEGLYCYSAPHESERIALAIALAMETLEUALAARGARGGLU	145
Db	367	GGAAAGCCCATCGCCTTTGGGTGCTTCTCTGCGCCCGCCGATCATCGCCAAAGCGGAGGAG	426
QY	146	TYRLEUTYRLEUGLYGLYLEUUSERSERGLYVALSERLEUAPHEPTRLEUHSIPHE	165
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Db	487	GTCAAGTCCCATCTTTGGCCACACTCTCTCGGACGCTTCATGTTTAGAGTTTACTTTGGCTG	546
QY	186	LEUVALPHEVALGLYTRYLLEVALPHEASPTHRINGLULEILEGLULYSALAHISLEU	205
Db	547	TTGATCTTCTCTGGGGTACATGTTGTACAGACGAGAGATCATCGAAGAGGGCCGACCAT	606
QY	206	GLYASPHETSPYRVALYSHISALALEUHRLEUPHEPTRAPAPHEGLYALAPHE	225
Db	607	GGCAGCATGAGCATCATCAACAGAGCCCTCACCTTCACCGAGCTTTGTCGCTCTGC	666
QY	226	VALARGILEULEUILLIEMETLEULYSASNALASERGLYGLULYSILYSILYS	245
Db	667	GTCGAGTCCATCATCATCATCTCTCAAGAACGAGGCGACCAAGTGCGAGACAGAAAGAG	726
QY	246	ARGARG 247	
Db	727	AGGAAG 732	
RESULT 11			
AX660456		750 bp	DNA
LOCUS			linear
DEFINITION	Sequence 813 from Patent WO03000906.		PAT 22-MAR-2003
ACCESSION	AX660456		
VERSION	AX660456.1		GI:29162227
KEYWORDS			
SOURCE			
ORGANISM	Oryza sativa		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.		
REFERENCE	1		
AUTHORS	Glazebrook,J., Briggs,S., Cooper,B., Goff,S.A., Moughamer,T., Katagiri,F., Kreps,J., Provart,N., Ricke,D. and Zhu,T.		
TITLE	Plant disease resistance genes		
JOURNAL	Patent: WO 03000906-A 813 03-JAN-2003;		
FEATURES	Syngenta Participations AG (Ct)		
source	Location/Qualifiers		
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ORIGIN			
Alignment Scores:			
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Score:	876.50	Matches:	165
Percent Similarity:	82.33%	Conservative:	40
Best Local Similarity:	66.27%	Mismatches:	43
Query Match:	68.91%	Indels:	1
DB:	6	Gaps:	1
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QY	1	1	MetGluGlyPheThrSerPheHepAsperGlnSerAlaSerArgAsnArgTrpSerIyr 20
Db	1	ATGGAGCCCTCTTACTACCTCTGTCGGAGTACGAGAGCGGCGAGCGGGCTGACTAC 60	

OY		2	Aspergillus niger PhaeoGlu1 SerProLeuVal GlnThrHisLysGlyAla Val	40
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OY		41	TyrIleuthrLeucyScysAlaleuValAlaSerAlalaglalyatryLeuHnSileu	60
Dd		121	TACCTGAACAATACTGGTGCCGTGGCTGCGGCGGGGCGCATCTGACGTGGCC	180
OY		61	TrpaSnlleglglyLeulleutThrThrmelaIadysmetgLyserMetValTrpleu	80
Dd		181	TTGAACATCGCGGGAGATTGTACATGCTCGGGGCGGAGAACATCGCTGTGTTC	240
OY		81	SerAlaPropotyArgInglnglbnlysArvalAlaleuemetalalaAleupe	100
Dd		241	TCGGTGCTGCTCTTTGAGAAGAGAACAGTTTTGGATCTCTTGCGCCGTGCTGTG	300
OY		101	GluGlyAlaSerlleeglyProleuIleGluleuglyleaSnpheasPioserlleVal	120
Dd		301	GAAGGGGCTTAGTGGGCGCTCTGATCAAGCTCTGCTAGACTTTGACTCACTTCCT	360
OY		121	PheGlyAlapheValGlyCyAlaValValPheGlyCySpheSerAlalAlametu	140
Dd		361	GTACACGATTTGTTGGAACCTGCCATTCATT766gtcttccacttgcgccaattcgtt	420
OY		141	AlaararGARargJuttyrLeutyrtLeuglylglyLeuSerSergilyValSerleu	160
Dd		421	GCCAAGCTTAAGAGATTACCCTACCTGGTGGTGGTTCCTCTTCGGCTCTCCATCTG	480
OY		161	PhetrpleuHispheAlaSerSerllePheGlylglySerMetalValPheLysPheGlu	180
Dd		481	CTCTGGCGCATTTGGCCGCATCCATCTTTGGCACCTCCACCGGCGAGCTTCATGTTTAG	540
OY		181	LeuryrrPheglyLeulleuValPheValaglyrrtleValPheaspThrhgnlle	200
Dd		541	GTTTACTTTGGCTCTGATTATCTCTCGGGGATCAAGGATGATAGACACCGAGATATATC	600
OY		201	GluIylsAlahisLeuGIYAspMeetaspTyralySHisAlaleuThrlenPethrasp	220
Dd		601	GAGAGAGCTACACACGAGTACATGACATCAATCAAAGCAGCAGCTACCTTTCACCTAC	660
OY		221	PheGlyAlavalPheValarglleLeullelleketLeuLysASnAlaserGluLys---	239
Dd		661	TYTCGGCGCCGCTCTTGCGGATCTCGTCAICATGCTCAAGAAAGCGSTCTGACAAAGCG	720
OY		240	GluGluLysLysLysLysARGarasn	248
Dd		721	GAGGAGAAAGAGAGSAGAGAGGTCT	747
RESULT 12				
AB025926			1181 bp mRNA linear PLN 04-MAR-2006	
LOCUS				
DEFINITION			Oryza sativa Bt-1 mRNA for Bax inhibitor-1, complete cds.	
ACCESSION			AB025926	
VERSION			AB025926.3 GI:7209771	
KEYWORDS			Bax inhibitor-1.	
SOURCE			Oryza sativa	
ORGANISM			Oryza sativa	
			Eukaryota; Vitridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
			Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
			Ehrhartoidae; Oryzaceae; Oryza.	
REFERENCE			1 (sites)	
AUTHORS			Kawai,M., Pan,L., Reed,J.C. and Uchimiya,H.	
TITLE			Evolutionally conserved plant homologue of the Bax inhibitor-1	
			(Bt-1) gene capable of suppressing Bax-induced cell death in	
JOURNAL			YEAST(1)	
MEDLINE			FEB8 Lett. 464 (3), 143-147 (1999)	
PUBMED			20086876	
REFERENCES			2 (bases 1 to 1181)	
AUTHORS			Kawai,M. and Uchimiya,H.	
TITLE			Direct Submission	
JOURNAL			Submitted (06-Apr-1999). Hirofumi Uchimiya, University of Tokyo,	

Bunkuo-ku, Tokyo 113-0032, Japan  
(E-mail: uchimiya@imcbs.iam.u-tokyo.ac.jp, Tel: 81-3-3812-2910,  
Fax: 81-3-3812-2910)  
On Mar 8, 2000 this sequence version replaced gi:6759252.  
Sequence updated (02-Mar-2000).

FEATURES  
Location/Qualifiers

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/strain="Yamahoushi"  
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/protein\_id="BAA89540.3"  
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CVLAASAVGAYLHVNLGMLTGLGVSGSIAMLFVSPVFEERKRGILLAALEEG  
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LMLOFAASIFGHSIGMEVEYFGLIFLYWYDQEIIEERAHGDMYIKHALFL  
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BASE COUNT 262 a 295 c 317 g 307 t  
ORIGIN

Alignment Scores:  
Pred. No.: 1.27e-79 Length: 1181  
Score: 876.50 Matches: 165  
Percent Similarity: 82.33% Conservative: 40  
Best Local Similarity: 66.27% Mismatches: 43  
Query Match: 68.91% Indels: 1  
DB: 8 Gaps: 1

US-09-955-526-4 (1-248) x AB025926 (1-1181)

QY 1 MetGluGlyPheThrSerPheAspSerGlnSerAlaSerArgAsnArgTyrSerTyr 20  
DB 126 ATGGACGCTTCTACTCGACCTCGTGGCGTACGAGCGGCGGCGGCGTGGGCTAC 185  
QY 21 AspSerLeuLysAsnPheArgGlnSerProLeuValGlnThrHisLeuLysGlnVal 40  
DB 186 GACTCGCTGAAGAACTTCGCGACATCTCCCGCGCTCCAGTCCACCTCAAGCTCGTT 245  
QY 41 TyrLeuThrLeuLysCysAlaLeuValAlaSerAlaGlyAlaTyrLeuHisLeu 60  
DB 246 TACCTGACACATATGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 305  
QY 61 TrpAsnIleGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80  
DB 306 TTGAACATCGCGGATCTTACTATGCTCGGCTCGTGGGAGCATCGCTGGTGTTC 365  
QY 81 SerAlaProProTyrGlnGluGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100  
DB 366 TCGTGGCTGCTTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 425  
QY 101 GluGlyAlaSerIleGlyProLeuIleGlyIleAsnPheAspProSerIleVal 120  
DB 426 GAAGGGGCTTCAGTGGGCTCTGATCAAGCTGCTGTAGACTTTCACCTCAAGCATCTC 485  
QY 121 PheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaMetLeu 140  
DB 486 GTAACAGCATTTGTTGAAGTGCATTCATTCATTCATTCATTCATTCATTCATTC 545  
QY 141 AlaArgArgGluTyrLeuTyrLeuGlyLeuLeuSerSerGlyValSerLeuLeu 160  
DB 546 GCCAAGCGTAGGAGTACCTCTACCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 605  
QY 161 PheTrpLeuHisPheAlaSerIlePheGlyGlySerMetAlaValPheLysPheGlu 180  
DB 606 CTCTGGCTGAGTTTGGCGATCCATCTTTGGCCACTCCACCGGAGCTTCATGTTGAG 665

QY 181 LeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluIleLeu 200  
DB 666 GTTTCATTGGCTGTGTAICTTCTGGGTACATGGGTATGACACGAGGAGATCATC 725  
QY 201 GluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThrAsp 220  
DB 726 GAGAGGGCTCACCACGGTGACATGACTACATCAAGCAGCAGCTCACCTCTTCACTGAC 785  
QY 221 PheGlyAlaValPheValArgIleLeuIleMetLeuLysAsnAlaSerGluLys--- 239  
DB 786 TTTCGTGGCGCTCTTTCGGGATCCGTCATCATGCTCAAGAACCGGCTGACAACTCG 845  
QY 240 GluLysLysLysLysLysArgArgAsn 248  
DB 846 GAGGAGAAGAAGAGAGAGAGAGAGGCTCT 872  
RESULT 13  
AX660801 1137 bp DNA linear PAT 22-MAR-2003  
LOCUS  
DEFINITION Sequence 1158 from Patent WO03000906.  
ACCESSION AX660801  
VERSION AX660801.1 GI:29162565  
KEYWORDS  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM  
Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooideae; Triticeae; Triticum.  
REFERENCE  
1 Glazebrook, J., Briggs, S., Cooper, B., Goff, S.A., Moughamer, T.,  
Katagiri, F., Kreps, J., Provart, N., Ricke, D. and Zhu, T.  
TITLE Plant disease resistance genes  
JOURNAL Patent: WO 03000906-A 1158 03-JAN-2003;  
SYNGENTA PARTICIPATIONS AG (CH)  
FEATURES  
Location/Qualifiers  
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/organism="Triticum aestivum"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4565"  
BASE COUNT 224 a 318 c 324 g 271 t  
ORIGIN  
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Pred. No.: 5.47e-73 Length: 1137  
Score: 811.00 Matches: 165  
Percent Similarity: 79.76% Conservative: 36  
Best Local Similarity: 65.48% Mismatches: 45  
Query Match: 63.76% Indels: 6  
DB: 6 Gaps: 0  
US-09-955-526-4 (1-248) x AX660801 (1-1137)  
QY 2 GluGlyPheThrSerPheAspSerGlnSerAlaSerArgAsnArgTyrSerTyrAsp 21  
DB 99 CAGGAGATGACGCCCTTCTACTCGCTCGTGGCGGCGGAGGAGTGGGCTACGAC 158  
QY 22 SerLeu-LysAsnPhe-ArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 41  
DB 159 TCGCTTCAAGAACTTCGGGGAGATCTCCCGCGCTGCAAGCCCACTCAAGCTGTTT 218  
QY 41 TrpLeuThrLeuLysCysAlaLeuValAlaSerAlaAlaGlyAlaTyr--LeuHisIleLeu 60  
DB 219 ACCCTGACCTATGCTTTCCTCGCTCATCTGCGTGGGCTTAACTGACATG 278  
QY 60 euTrpAsnIleGlyLeuLeuThrThrMet-AlaCysMetGlySerMetValTrpLeu 79  
DB 279 CCCTGAACATCGTGGGATGCTGACAACTTTCGCTGTATCGGACCACTGCTGGATG 338  
QY 80 LeuSerAlaProProTyrGlnGluLysArgValAlaLeuLeuMetAlaAlaLeu 99  
DB 339 TACTCTGTCACCTCTATGAGGAGAGAGAGAGTGGGCTGCTGATGGGTGACGCCCTC 398  
QY 100 PheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIle 119

Db	61	GACTCGCTGAGAACTTCCGCCAGTATCTCCCGCGCGTCCAGCTCCACCTCAAGCTCGTT	120
Qy	41	TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu	60
Db	121	TACCTGACACTATGCTGCCTGCCCTGCGTGGCGGTGGCGCATACCTGCAGCTGCC	180
Qy	61	TrpAsnIleGlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeu	80
Db	181	TTGACATATCGCGGATGTTGACTATGCTGGGTGCGTGGGAGCATCGCTGTGTTC	240
Qy	81	SerAlaProProTyrGlnGlu-----Gln-LysArgValAlaLeuLeuMetAlaAla	98
Db	241	TCGGTGCCTGCTTTGAGAGTGCAGCAGAGGAAGAGTTGGGATCTCTTGGCGGTGC	300
Qy	98	AlaLeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAsp--Pro	117
Db	301	CTTGCTGGAAGGGCTTCAGTTGGGCTCTGATCAAGCTTGTCTGTAGACTTTGACTCAAG	360
Qy	118	SerIleValPheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAla	137
Db	361	AGCATTCCTGTAACACCAATTGTTGAACTGCCATTTCGCTTCATTTCGCT	420
Qy	138	AlaMetLeuAlaArgArgGluTyrLeuTyrLeuGlyGlyLeuSerSerGlyVal	157
Db	421	GCCATCGTTGCCAAGGATAGGAGTACCTACCTTGGTGGTTTGCTCTTCTTGGCCCTC	480
Qy	158	SerLeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPhe	177
Db	481	TCCATCTGCTGCTGGCTGCAGTTGGCGCATCCATCTTTGGCCACTCCACGGCAGCTTC	540
Qy	178	LysPheGlu---LeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThr	196
Db	541	ATGTTTTCAGCAGGTTTACTTTGGCCCTGTCATCTCTCGGGTACATGGTGTATGACAG	600
Qy	197	GlnGluIleGluLysAlaHisLeuGlyAspMetAspTyrValIysHisAlaLeuThr	216
Db	601	CAGAGATCATCGAGAGGCTCACCAGGTGACATGGACTACATCAAGCAGCACTCACC	660
Qy	217	LeuPheThrAspPheGlyAlaValPheValArgIleLeuIleMet-LeuLysAsnAl	236
Db	661	CTCTTCACTGACTTCGTGGCGCTCTTGTCCGGATCTCGTCAATCATGTGCTCAAGACGC	720
Qy	236	aSerGluLys---GlnGluLysLysLysLysArgArgAsn	248
Db	721	GTCGTCAAGTTCGGAGGAGAGAGAGAGAGAGAGGTCT	760
RESULT 15			
LOCUS	AX660870	750 bp	DNA
DEFINITION	Sequence 1227 from Patent WO03000906.	linear	PAT 22-MAR-2003
ACCESSION	AX660870		
VERSION	AX660870.1	GI:29162634	
KEYWORDS			
SOURCE	Zea mays		
ORGANISM	Zea mays		
REFERENCE			
AUTHORS	Glazebrook,J., Briggs,S., Cooper,B., Goff,S.A., Moughamer,T., Katagiri,F., Kreps,J., Provart,N., Ricke,D. and Zhu,T.		
TITLE	Plant disease resistance genes		
JOURNAL	Patent: WO 03000906-A 1227 03-JAN-2003;		
SYNOPSIS	Syngenta Participations AG (CH)		
FEATURES	Location/Qualifiers		
source	1..750		
BASE COUNT	130 a	233 c	200 g
ORIGIN			187 t
Alignment Scores:			

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Percent Similarity: 78.69% Conservative: 34
Best Local Similarity: 64.75% Mismatches: 45
Query Match: 61.83% Indels: 7
DB: Gaps: 3

US-09-955-526-4 (1-248) x AX660870 (1-750)

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QY 28 GlnIleSerProLeuValGlnThrHisLeuLysGlnValTyrLeuThrLeuCysCysAla 47
DB 79 CACATCTCACCGCGTGTGACATCCCAACATGTACCTCAACCTCAACCTCGAGGCGCGT 138
QY 48 LeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrpAsnIleGlyLeuLeu 67
DB 139 CTGGCGCTTCTGCACTCGCGGCTACCTCCATCTCTCAACCTCGAGGCGCGCTC 198
QY 68 ThrThrMetAlaCysMetGlySerMetValTrpLeuLeuSerAlaProTyr----- 85
DB 199 ACGACGGTGGGTGGTGGCTCCATCGGCTTCCTCATCTCCTGCGCGCTCACGGAC 258
QY 86 GlnGluGlnLysArgValAlaLeuLeuMetAlaAlaLeuPheGluGlyAlaSerIle 105
DB 259 CAGGAGAGGAACCGCTTGGCGTGTCTCATGTCTGCGCGCTCTTCAAGCGCGTCCGTT 318
QY 106 GlyProLeuIleLeuGlyLeuAsnPheAspProSerIleValPheGlyAlaPheVal 125
DB 319 GGTCCGCTCGTGCACCTGTTATGACTGGATTTCAGGATTCTCTCATCTGCGTTCGTC 378
QY 126 GlyCysAlaValValPheGlyCysPheSerAlaAlaAlaMetLeuAlaArgArgGlu 145
DB 379 GGGACCGCAGTTCTTTGCATGCTTCTGGCGCTGCCATCATCCCAAGCGCGAGAA 438
QY 146 TyrLeuTyrLeuGlyLeuLeuSerSerGlyValSerLeuLeuPheTrpLeuHisPhe 165
DB 439 TACTCTACCTCGCGGCTGTGTTTTCATCTGGCTCTCCATCTCTCTGCTGCAGTTT 498
QY 166 AlaSerSerIlePheGlyGlySerMetAlaValPheIlePheGlyLeuTyrPheGlyLeu 185
DB 499 GCTACTTCATCTTTGGCCACACCGCGGACCTTCATGTTGAGCTCTACTTGGCCIC 558
QY 186 LeuValPheValGlyTyrIleValPheAspThrGlnGluIleIleGluLysAlaHisLeu 205
DB 559 CTGGTTTCTGGGATATATGTTGTTGACACCCAGGAGATCATCGAGGGCGCACCGGT 618
QY 206 GlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThrAspPheGlyAlaValPhe 225
DB 619 GGGGACATGACATACATCAAGCAGCGGCTGACTCTCTTCAACGACTTGTGCGGTCTT 678
QY 226 ValArgIleLeuIleIleMetLeuLysAsnAlaSerGluLys-----GluGluLysLys 243
DB 679 GTTCGATCTCTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 738
QY 244 LysLysArgArg 247
DB 739 AGGAAGAAGCGG 750

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Search completed: September 22, 2003, 16:21:15  
Job time : 2822 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 22, 2003, 15:21:58 : Search time 267 Seconds  
(without alignments)  
2507.343 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272

Sequence: 1 MEGFTSFDSQASNRWSY.....LIIMKNASERKKKKRN 248

Scoring table:

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Fgapop 6.0	Fgapext 7.0	
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Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LIST=45 -DOCALIGN=200 -THR\_SCORE=opt -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
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Database : N\_Geneseq\_19Jun03:\*\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1027.5	80.8	1009	24	ABN98455
2	1004.5	79.0	1066	21	AAC38715
3	688.5	54.1	884	22	AAF44782
4	499.5	39.3	527	22	AAF44783
5	492.5	38.7	712	21	AAC51940
6	491.5	38.6	873	22	AAF92293
7	483.5	38.0	2922	21	AAF18054
8	483.5	38.0	2994	25	ABX63356
9	479.5	37.7	2634	19	AAV59067
10	473.5	37.2	2600	24	ABK84658
11	426	33.5	376	25	ABX19768
12	382.5	30.1	751	24	ABQ56073
13	371.5	29.2	536	24	ABV88094
14	312	24.5	1085	23	ABL12505
15	310.5	24.4	638	23	ABV23317
16	305	24.0	520	20	AAV86028
17	296	23.3	251	25	ABX25165
18	285	22.4	410	25	ABX43279
19	275.5	21.7	595	24	ABQ59227
20	272.5	21.4	380	21	AAC04218
21	269	21.1	3775	23	ABL12504
22	256.5	20.2	689	24	ABQ60318
23	255	20.0	257	25	ABX24245
24	219	17.2	392	25	ABX43548
25	219	17.2	431	25	ABX48159
26	192	15.1	1359	23	ABL02337
27	192	15.1	3359	23	ABL02336
28	191	15.0	463	21	AAC03759
29	188	14.8	601	21	AAA16226
30	172	13.5	1198	23	ABL03963
31	171	13.4	2475	21	AAC86459
32	165	13.0	1035	21	AZ48818
33	165	13.0	1038	25	ABZ75900
34	165	13.0	1268	21	AZ48819
35	165	13.0	1316	21	AZ58548
36	165	13.0	1355	24	ABK35731
37	165	13.0	1394	20	AAV73001
38	165	13.0	1394	24	ABQ92026
39	165	13.0	1429	25	ABZ75907
40	165	13.0	1596	19	AAV59684
41	165	13.0	1596	24	ABZ73671
42	165	13.0	1714	20	AZ77497
43	165	13.0	1943	21	AZ64941
44	165	13.0	1943	22	AAF44087
45	165	13.0	1943	24	ABK69961

## ALIGNMENTS

### RESULT 1

ABN98455  
ID ABN98455 standard; DNA; 1009 BP.

AC ABN98455;

XX 01-AUG-2002 (first entry)

DT Arabidopsis thaliana expressed polynucleotide SEQ ID NO 223.

DE Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;  
KW disease; crop; thale cress; tolerance factor; insect; pathogen;  
KW nutrition; ds.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

XX US2002023281-A1.

FN



DT	17-OCT-2000	(first entry)
XX	Arabidopsis	thaliana DNA fragment SEQ ID NO: 21973.
XX		
XX		
KW	Hybridisation assay;	genetic mapping; gene expression control;
KW	protein identification;	signal transduction pathway;
KW	metabolic pathway;	promoter; termination sequence; ss.
XX		
XX	Arabidopsis	thaliana.
OS		
XX	EP1033405-A2.	
PN	06-SEP-2000.	
PD		
XX		
PF	25-FEB-2000;	2000EP-0301439.
XX		
PR	25-FEB-1999;	99US-0121825.
PR	03-MAR-1999;	99US-0123180.
PR	09-MAR-1999;	99US-0123548.
PR	23-MAR-1999;	99US-0125788.
PR	25-MAR-1999;	99US-0126264.
PR	29-MAR-1999;	99US-0126785.
PR	01-APR-1999;	99US-0127462.
PR	08-APR-1999;	99US-0128234.
PR	08-APR-1999;	99US-0128714.
PR	16-APR-1999;	99US-0129845.
PR	19-APR-1999;	99US-0130077.
PR	21-APR-1999;	99US-0130449.
PR	23-APR-1999;	99US-0130510.
PR	23-APR-1999;	99US-0130891.
PR	28-APR-1999;	99US-0131449.
PR	30-APR-1999;	99US-0132048.
PR	30-APR-1999;	99US-0132407.
PR	04-MAY-1999;	99US-0132484.
PR	05-MAY-1999;	99US-0132485.
PR	06-MAY-1999;	99US-0132486.
PR	06-MAY-1999;	99US-0132487.
PR	07-MAY-1999;	99US-0132863.
PR	11-MAY-1999;	99US-0134256.
PR	14-MAY-1999;	99US-0134218.
PR	14-MAY-1999;	99US-0134219.
PR	14-MAY-1999;	99US-0134221.
PR	14-MAY-1999;	99US-0134370.
PR	18-MAY-1999;	99US-0134768.
PR	19-MAY-1999;	99US-0134941.
PR	20-MAY-1999;	99US-0135124.
PR	21-MAY-1999;	99US-0135353.
PR	24-MAY-1999;	99US-0135629.
PR	25-MAY-1999;	99US-0136021.
PR	27-MAY-1999;	99US-0136392.
PR	28-MAY-1999;	99US-0136782.
PR	01-JUN-1999;	99US-0137222.
PR	03-JUN-1999;	99US-0137528.
PR	04-JUN-1999;	99US-0137502.
PR	07-JUN-1999;	99US-0137724.
PR	08-JUN-1999;	99US-0138094.
PR	10-JUN-1999;	99US-0138540.
PR	10-JUN-1999;	99US-0138847.
PR	14-JUN-1999;	99US-0139119.
PR	16-JUN-1999;	99US-0139452.
PR	16-JUN-1999;	99US-0139453.
PR	17-JUN-1999;	99US-0139492.
PR	18-JUN-1999;	99US-0139454.
PR	18-JUN-1999;	99US-0139455.
PR	18-JUN-1999;	99US-0139456.
PR	18-JUN-1999;	99US-0139457.
PR	18-JUN-1999;	99US-0139458.
PR	18-JUN-1999;	99US-0139459.
PR	18-JUN-1999;	99US-0139460.
PR	18-JUN-1999;	99US-0139461.
PR	18-JUN-1999;	99US-0139462.
PR	18-JUN-1999;	99US-0139463.
PR	18-JUN-1999;	99US-0139750.





```

PT forestry plant -
XX
PS
XX
XX Claim 1; Page 62; 142pp; English.
CC The present invention relates to coding sequences (see AAF44740-F44840
and AAF4843-F44844) and proteins (see AAB65714-B65814) involved in
CC programmed cell death (PCD; apoptosis). The coding sequences and proteins
CC of the present invention are useful for modulating a PCD or cell death
CC pathway and various developmental pathways in a forestry plant, by
CC stably incorporating one of the present coding sequences into the genome
CC of the forestry plant, where the coding sequence provides a PCD pathway
CC that is not present in a native form of the forestry plant.
XX
SQ Sequence 884 BP; 219 A; 165 C; 216 G; 284 T; 0 other;

Alignment Scores:
Pred. No.: 1,04e-71 Length: 884
Score: 688.50 Matches: 137
Percent Similarity: 79.25% Conservative: 31
Best Local Similarity: 64.62% Mismatches: 41
Query Match: 54.13% Indels: 3
DB: 22 Gaps: 2

US-09-955-526-4 (1-248) x AAF44782 (1-884)
QY 39 GlnValTyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHis 58
Db 2 AGGGTTTATTGTCGCTTAGCTGTCCTCGTAACAGCAGCGATCGTGTATTATTTGCAT 61
QY 59 IleLeuTrpAsnIleGlyLeuLeuThrMetAlaCysMetGlySerMetValTrp 78
Db 62 CTCTCTGTAATATTGGAGGGCTCTCAGCGGGCTCGCTTGCATGCTGTCTAATCGGG 121
QY 79 LeuLeuSerAlaPro-----ProTyrGlnGluGlnLysArgValAlaLeuMetAla 96
Db 122 CTTCTATCCGTCCTACTCTCGAACATGAGGGTAAGAGAGCTCGCTGCTCTTCGGCA 181
QY 97 AlaAlaLeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAsp 116
Db 182 GCTGCTGCTTCAAGGGAGCTACTCTGGGACCGCTCATCGACGCGCTCATTAATATTGAC 241
QY 117 ProSerIleValPheGlyAlaPheValGlyCysAlaValAlaPheGlyCysPheSerAla 136
Db 242 TCCAGTATATCTGGTAGTCGCTTGTGGACCTCTTGGCCTTCGCTTTCGGCA 301
QY 137 AlaAlaMetLeuAlaArgArgGluTyrLeuTyrLeuGlyLeuLeuSerSerGly 156
Db 302 GCAGCAATCACAGCCAGGAGCGGGAATACCTATTTTGGGAGGATATTGGGCTCGGA 361
QY 157 ValSerLeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlySerMetAlaVal 176
Db 362 ATCAGCATATTGATGTGGTGTCAACTAGCATCTCGATTTTGGTGGTCTTCGCGGATT 421
QY 177 PheLysPheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThr 196
Db 422 TACACATTTGAGATCTACCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481
QY 197 GlnGluIleGluLysAlaHisLysLysAspMetAspTyrValLysHisAlaLeuThr 216
Db 482 CAGATCATCATCAGAAAGCGGACCATGGAGACTATGATTAATTAACATTCACCTGGAC 541
QY 217 LeuPheThrAspPheGlyAlaValPheValArgIleLeuIleLeuMetLeuLysAsnAla 236
Db 542 CTCTTCATTGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
QY 237 ---SerGluLysGluLysLysLysLysArgArg 247
Db 602 GACAGTAATATCCAGGGAAGGAAAGAGAGAGAG 637

RESULT 4
AAF44783
ID AAF44783 standard; cDNA; 527 BP.
XX

```

```

AC AAF44783;
XX
DT 27-MAR-2001 (first entry)
XX
DE Testis Enhanced Gene Transcript protein coding sequence #2.
XX
KW Cell death modulator; programmed cell death; PCD; apoptosis;
KW forestry plant; ss.
XX
OS Pinus radiata.
XX
PN WC200075331-A1.
XX
XX 14-DEC-2000.
XX
XX 02-JUN-2000; 2000WO-NZ00086.
XX
XX 04-JUN-1999; 99US-0325932.
XX
XX (GENF-) GENESIS RES & DEV CORP LTD.
XX
XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
XX Flinn B, Lasham A;
XX
XX WPI; 2001-061724/07.
XX
XX P-PSDB; AAB65756.
XX
XX Novel defender against cell death polynucleotide useful for modulating
XX programmed cell death pathway and specific development pathways in
XX forestry plant -
XX
XX Claim 1; Pages 62-63; 142pp; English.
XX
XX The present invention relates to coding sequences (see AAF44740-F44840
and AAF4843-F44844) and proteins (see AAB65714-B65814) involved in
XX programmed cell death (PCD; apoptosis). The coding sequences and proteins
XX of the present invention are useful for modulating a PCD or cell death
XX pathway and various developmental pathways in a forestry plant, by
XX stably incorporating one of the present coding sequences into the genome
XX of the forestry plant, where the coding sequence provides a PCD pathway
XX that is not present in a native form of the forestry plant.
XX
XX Sequence 527 BP; 98 A; 148 C; 143 G; 138 T; 0 other;

Alignment Scores:
Pred. No.: 1.25e-49 Length: 527
Score: 499.50 Matches: 101
Percent Similarity: 79.72% Conservative: 13
Best Local Similarity: 70.63% Mismatches: 26
Query Match: 39.27% Indels: 4
DB: 22 Gaps: 1

US-09-955-526-4 (1-248) x AAF44783 (1-527)
QY 1 MetGluGlyPheThrSerPheAspSerGlnSerAlaSerArgAsnArgTrpSerTyr 20
Db 107 ATGGACGCGTTCGCTTCCCTGCTCCAGTCG-----AGCGCAAGGGGTGGAGCCAC 157
QY 21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40
Db 158 GATTCCCTCAAGAACTTCGCCAGATATCTCCGCCGATATCTCCGCTCAATCTCACCACAGATGTT 217
QY 41 TyrLeuThrLeuCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60
Db 218 TATCTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 277
QY 61 TrpAsnIleGlyLeuLeuThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
Db 278 CTGAACATCGCGGGCTCTCAGACAAATGCTTGCATCGAAGACATCGTGTGGCTGCTT 337
QY 81 SerAlaProProTyrGlnGluGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100
Db 338 TCGATTCTCCATGAAGAGAAAGAGTTGGTGTGCTCATGGCGGCGCTCTCTT 397

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```
QY 101 GluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspSerIleVal 120
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 398 GAAGGAGCGTATCGGTCTCTCATCGAAGCGGCAITTAAGTCGACCGGCAITGTG 457
QY 121 PheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaMetLeu 140
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 458 ATAAGCGCATTTGTGGATCTGCGTGGCTTGTCTGCGGCGCAGC-ATGTTG 516
QY 141 AlaArgArg 143
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 517 GCTAGCGG 525

RESULT 5
AAC51940
ID AAC51940 standard; DNA; 712 BP.
XX
AC AAC51940;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 70058.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
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PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
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PR 18-JUN-1999; 99US-0139458.
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PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
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PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
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PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
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PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
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PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149175.  
PR 17-AUG-1999; 99US-0149426.  
PR 18-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 06-OCT-1999; 99US-0157753.  
PR 07-OCT-1999; 99US-0157865.  
PR 08-OCT-1999; 99US-0158029.  
PR 12-OCT-1999; 99US-0158232.  
PR 13-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 18-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Alignment Scores:  
Pred. No.: 1-31e-48  
Score: 492.50

Length:  
Matches: 712  
90

Percent Similarity: 87.30% Conservative: 20  
Best Local Similarity: 71.43% Mismatches: 15  
Query Match: 38.72% Indels: 1  
DB: 21 Gaps: 1  
US-09-955-526-4 (1-248) x AAC51940 (1-712)  
QY 1 MetGluGlyPheThrSerPheAspSerGlnSerAlaSerArgAsnArgTrpSerTyr 20  
Db 40 ATGGATCGGTTCTCTTCCTTCATACCTGGTAGCAGAACG---TGGACCTAT 96  
QY 21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40  
Db 97 GATTCTCTTAAAAAATTCGTCAGATTCTCCAGCGGTTCCAGAAATCATCTTAAACGGGT 156  
QY 41 TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60  
Db 157 TATTTGACCTTATGTTGTCTCTGTGGGCTTCGCTTTGGAGCTTACCTCCATGTGCTC 216  
QY 61 TrpAsnIleGlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80  
Db 217 TGGATATCGCGGTATCTTACACGATGGATGATTGGAACTATGATTGGCTCCTT 276  
QY 81 SerAlaProProTyrGlnGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100  
Db 277 TCATGTCCCTCTTATGACACCAAAAAGGCTTCTCTCTGTTGCGTCTGCTGTTCT 336  
QY 101 GluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleVal 120  
Db 337 GAAGGTGCTCTGTGGCCCTTGATCAAGTGGCAATTGATGTACCCAGCATCCTT 396  
QY 121 PheGlyAlaPheValGly 126  
Db 397 ATCACTGCGTGTGTGGA 414  
RESULT 6  
AAF92293  
ID AAF92293 standard; cdna; 873 BP.  
XX  
AC AAF92293;  
XX  
DT 15-MAY-2001 (first entry)  
XX  
DE Bovine mammary tissue derived cdna #6.  
XX  
KW Bovine; mammary gland; cancer; tumour; angiogenesis; ss.  
XX  
OS Bos taurus.  
XX  
PN WO200114553-A1.  
XX  
PD 01-MAR-2001.  
XX  
PF 23-AUG-2000; 2000WO-NZ00166.  
XX  
PR 23-AUG-1999; 99US-0150330.  
XX  
{GENE-} GENESIS RES & DEV CORP LTD.  
PA (NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.  
XX  
PI Havukkala IJ, Gleen M, Grigor MR, Molenaar AJ;  
XX  
DR WPI; 2001-226619/23.  
XX  
PT New polypeptides and polynucleotides encoding the polypeptides, which  
PT are expressed in bovine mammary gland tissue, useful for stimulating  
PT mammary gland growth or function, or inducing differentiation of milk  
PT producing cells  
XX  
XX  
PS Claim 1; Page 43; 97pp; English.  
XX  
CC The present invention relates to proteins derived from bovine  
CC mammary gland cells. The invention is useful for stimulating

CC bovine mammary gland cell growth and function, inhibiting the  
CC growth of various mammary gland cancer cells, inhibiting  
CC angiogenesis and vascularization of tumours, or modulating  
CC the growth of blood vessels in a mammal.

XX Sequence 873 BP; 206 A; 218 C; 196 G; 253 T; 0 other;

## Alignment Scores:

Pred. No.: 2,31e-48 Length: 873  
Score: 491.50 Matches: 99  
Percent Similarity: 65.80% Conservative: 53  
Best Local Similarity: 42.86% Mismatches: 72  
Query Match: 38.64% Indels: 7  
DB: 22 Gaps: 4

US-09-955-526-4 (1-248) x AAF92293 (1-873)

QY 19 SerTyrAspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLys 38  
DB 55 AACTTTGATGCACTCTTTAAATTTCCACATAACCCCTCGACACGACGACCTGAAG 114  
QY 39 GlnValTyrLeuThrLeuLysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHis 58  
DB 115 AAGGTTATGCGCAGTTTCCCTCTGTATGTTGTGGGCTGGGGGCTATATCCAT 174  
QY 59 IleLeuTrpAsnIle-----GlyGlyLeuLeuThrMetAlaCysMetGlySerMet 76  
DB 175 GTGGTCACCATTCATTCAGGCTGGCTCTCTCTGCTTGGGCTCTTGGGTTGATG 234  
QY 77 ValTrpLeuLeuSerAlaProTrpGln-----GluGlnLysArgValAlaLeuLeu 94  
DB 235 ATTGGCTGATGCACACCTCAGACCCATGAACAGTGCACAAAGACCTGGACCTCTG 294  
QY 95 MetAlaAlaLeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyLeuAsn 114  
DB 295 GCTGGATTGCTTCTTACAGAGTGGCTGGGCTGCTGGACTGTGTCATTCGC 354  
QY 115 PheAspProSerIleValPheGlyAlaPheValGlyCysAlaValPheGlyCysPhe 134  
DB 355 ATCAACCCGACGATCCTCCACCTGCTTCATGGGCGACAGCAATGATCTACCTGCTC 414  
QY 135 SerAlaAlaMetLeuAlaArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSer 154  
DB 415 ACCCTGAGTGCATCTATCCAGGCGCCGTAGTACTCTTCTAGAGGATCTTGATG 474  
QY 155 SerGlyValSerLeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlySerMet 174  
DB 475 TCGGCATGAGCTCATGCTC---TTGCTCTCCCTGGGGAACCTTTCTTCGATCTGT 531  
QY 175 AlaValPheLysPheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPhe 194  
DB 532 TGGCTTTTCCAGCAACCTGTATATGGGCTGGTGTGATGCTGCTTGTTCCTTTT 591  
QY 195 AspThrGlnIleIleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAla 214  
DB 592 GATACTCAACTCATTTTAAAGAGGCTGAAATGGAGATAAGATTATATCTGGCACTGC 651  
QY 215 LeuThrLeuPheThrAspPheGlyAlaValPheValArgIleLeuIleMetLeuLys 234  
DB 652 GTTGACCTCTCTTGGATTTCGTAACCTCTCTCAGAAAGCTCATGATGCTGGCTATG 711  
QY 235 AsnAlaSerGluLysGluGluLysLysLysLys 245  
DB 712 AAT-----CAGAGGATAGAGAGAGAGAG 738

## RESULT 7

AAFI8054

ID AAF18054 standard; DNA; 2922 BP.

XX

AC AAF18054;

XX

DT 14-MAR-2001 (first entry)

XX

DE XX  
KW Human; lung cancer associated polynucleotide sequence SEQ ID 73.  
KW cardioactive; immunomodulatory; muscular active; cytostatic;  
KW gastrointestinal; nephrotropic; antiinfective; gynecological;  
KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;  
KW proliferative disorder; wound healing; infectious disease; ds.  
XX Homo sapiens.  
XX WO2000055180-A2.  
XX 21-SEP-2000.  
XX 08-MAR-2000; 2000WO-US05918.  
XX 12-MAR-1999; 99US-0124270.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (ROSE/) ROSEN C A.  
XX Ruben SM;  
XX WPI: 2000-587514/55.  
XX P-PSDB; AAB58178.

PT Lung cancer associated gene sequences, referred to as lung cancer  
PT antigens, useful for treatment, prevention, and diagnosis of disorders  
PT such as lung cancer -  
XX Claim 1; Page 550-551; 1425pp; English.

XX Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer  
XX associated proteins represented in AAB58106 - AAB58548. Lung cancer  
XX associated proteins and polynucleotide sequences, their agonists, and  
XX antagonists may have neuroprotective; cytostatic; cardioactive;  
XX immunomodulatory; muscular active general; vulnary; gastrointestinal  
XX general; nephrotropic; antiinfective; gynecological; or antibacterial  
XX activity. The invention also includes antibodies specific for the  
XX protein or polynucleotide sequences. The lung cancer associated  
XX polynucleotide sequences may be used for detection of lung cancer,  
XX chromosome identification, as chromosome markers, and for numerous other  
XX diagnostic or research purposes. The proteins may be used to treat  
XX disorders such as neural, immune, muscular, reproductive,  
XX gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
XX disorders. The proteins may also be used in the treatment of wounds and  
XX infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and  
XX peptide AAB58549 are used in the course of the invention for the  
XX identification and characterisation of the polynucleotide and protein  
XX sequences.

XX SQ Sequence 2922 BP; 712 A; 686 C; 654 G; 863 T; 7 other;

## Alignment Scores:

Pred. No.: 1.19e-46 Length: 2922  
Score: 483.50 Matches: 102  
Percent Similarity: 62.90% Conservative: 54  
Best Local Similarity: 41.13% Mismatches: 79  
Query Match: 38.01% Indels: 13  
DB: 21 Gaps: 5

US-09-955-526-4 (1-248) x AAF18054 (1-2922)

QY 3 GlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyrAspSer 22  
DB 108 GGAACCATCAACATATTTGAT-----CGAAGATCAACTTTGATGCG 149  
QY 23 LeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyrLeu 42  
DB 150 CTTTTTAATTTTCTCATATAACCCGCTCAACCCAGCAGCAGCAGGAGGCTATGCA 209  
QY 43 ThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrpAsn 62  
DB 433

WPI; 2003-110597/10.

Combination for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, comprises several cDNAs that are differentially expressed in activated vascular tissue -

Claim 1; Page -; 18pp; English.

This invention relates to a combination comprising several cDNAs that are differentially expressed in activated vascular tissue. The invention also discloses a high throughput method for detecting differentially expressed cDNAs in a sample. The cDNAs of the invention may have antiatherosclerotic; cytostatic; cardiact; hypertensive; antidiabetic; gynaecological; vasotropic and cerebroprotective activities and may be used in gene therapy. The cDNAs of the invention may be used in a high-throughput methods for detecting differential expression of one or more cDNAs in a sample, or screening several molecules or compounds to identify a molecule or compound that specifically binds a cDNA of the invention. A protein encoded by the cDNA may be used to screen several molecules or compounds to identify a ligand that specifically binds to the protein, or to produce or purify an antibody to the protein that can be used to detect a protein in a sample or purify a natural or recombinant protein from a sample. The nucleotides may be useful for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, cancer, coronary artery disease, hypertension, diabetes, pre-eclampsia, ischaemia-reperfusion injury, stenosis, or stroke. The cDNAs can also be used for large-scale genetic or gene expression analysis of several new nucleic acid molecules. Antibodies to the proteins encoded by the cDNAs are useful for diagnosing pre-pathologic disorders, and chronic or acute diseases associated with abnormalities in the expression, amount or distribution of the protein. The present sequence represents a cDNA of the invention that is differentially expressed in activated vascular tissue.

Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly from USPTO at <http://seqdata.uspto.gov/sequence.html?docID=20020317081>.

## RESULT 8

Alignment Scores:			
Pred. No.:	1.23e-46	Length:	2994
Score:	483.50	Matches:	102
Percent Similarity:	62.90%	Conservative:	54
Best Local Similarity:	41.13%	Mismatches:	79
Query Match:	38.01%	Indels:	13
DB:	25	Gaps:	5
US-09-955-526-4 (1-248) x ABX63356 (1-2994)			
QY	3	GlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyAspSer	22
DB	229	GAACCATGACATATTGAT	270
QY	23	LeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyLeu	42
DB	271	CTTTTAAATTTTCTCATATAACCCGCTGACAGCAGCAGCACCTGAAGAAGTCTTATGCA	330
QY	43	ThrLeuCysCysAlaLeuValAlaSerAlaAlaClyAlaTyrlLeuHisIleLeuTrpAsn	62
DB	331	AGTTTGGCCCTTGTGATTTGTGGCGGCTGCAGGGGCCCTATGCCATATGGTCACTCAT	390
QY	63	Ile-----GlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu	80
DB	391	TTCAATTCAGGCTGGCTCTCTCGCTGGCTCCCTGATATGATTTGGCTGATG	450
QY	81	SerAlaProProTyrGln-----GluGlnLysArgValAlaLeuLeuMetAlaAla	98
DB	451	GCAACACCTCATAGCCATGAACATGAACAGAAAGACTGGGACTTCTTGCTGGATTGCA	510
QY	99	LeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSer	118

Db 511 TTCCTTACAGGAGTTGGCCCTGGCCCTGCCCTGGAGCTTTTGTATTGCTGTCAACCCGAGC 570  
 QY 119 IleValPheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaAla 138  
 Db 571 ATCCTCCACGACTCTTTCATGGCGCAGCGCAATGATCTTTACCTGCTCACCTCAGTGCA 630  
 QY 139 MetLeuAlaArgArgGluTyrLeuTyrLeuTyrLeuGlyLeuLeuSerSerGlyValSer 158  
 Db 631 CTCATGCCAGGCGCGTAGTACCTCTTCTGGAGGTATCTGTGATGTCAGCCCTGAGC 690  
 QY 159 LeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLys 178  
 Db 691 TTGTTGCTT---TTGCTCCCTGGGGAATGTTTCTTGGATCCATTGGCTTTCCAG 747  
 QY 179 PheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGlu 198  
 Db 748 GCAAACTGTATGTGGACTGGTGGTCAATGTCATGTGGCTTCTGTCCTTTTGATCTCACTC 807  
 QY 199 IleIleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPhe 218  
 Db 808 ATTATTGAAAAGGCCGCAACATGGAGATCAAGATTATATCTGGCAGCTGCATTGATCTCTC 867  
 QY 219 ThrAspPheGlyAlaValPheValArgIleLeuIleMetLeuLysAsnAlaSerGlu 238  
 Db 868 TTAGATTTCATTACTCTCTCAGAAACATCATGATGATCTGCGCATGAT---GAA 921  
 QY 239 LysGluGluLysLysLysArg 246  
 Db 922 AAGGATAAAGAAGAAGAAGAA 945  
 RESULT 9  
 AAV59067  
 ID AAV59067 standard; cDNA; 2634 BP.  
 AC AAV59067;  
 XX  
 DT 02-FEB-1999 (first entry)  
 XX  
 DE Bax inhibitor BI-1 cDNA.  
 KW Bax inhibitor; BI-1; human; apoptosis; ss.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 73..786  
 FT /\*tag= a  
 XX  
 PN WO9840397-A1.  
 XX  
 PD 17-SEP-1998.  
 XX  
 PF 13-MAR-1998; 98WO-0505015.  
 XX  
 PR 14-MAR-1997; 97US-0818514.  
 XX  
 PA (BURN-) BURNHAM INST.  
 XX  
 PI Reed JC, Xu Q;  
 XX  
 DR WPI; 1998-531519/45.  
 DR P-PSDB; AAW73136.  
 XX  
 PT Bax inhibitor proteins, BI-1 and BI-2 - useful e.g. to modulate  
 PT cellular apoptotic activity or identify agents altering BI-1 or BI-2  
 PT binding which can modulate apoptotic activity  
 XX  
 PS Claim 2; Page 61-63; 80pp; English.  
 XX  
 CC This cDNA clone codes for an inhibitor protein, termed BI-1 (see  
 CC AAW73136), of the pro-apoptotic protein Bax. Nucleic acids encoding  
 CC BI-1 and BI-2 (see AAV59068) were identified by suppression of  
 CC Bax-induced death of yeast cells transformed to express human Bax.

CC A human Hep62 cDNA library was used for library screening. The  
 CC invention provides vectors, optionally expression or viral vectors,  
 CC containing BI nucleic acids, and host cells containing these  
 CC vectors. The nucleic acids encoding BI-1/BI-2 can be used to  
 CC increase expression of these proteins in cells, or antisense  
 CC molecules prepared from them used to decrease expression. In  
 CC these ways, cellular apoptotic activity may be modulated (claimed).  
 CC The nucleic acids and complementary sequences are also useful as  
 CC probes to detect BI-encoding nucleic acid molecules in samples.  
 XX  
 XX Sequence 2634 BP; 632 A; 626 C; 597 G; 779 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 3,05e-46 Length: 2634  
 Score: 479.50 Matches: 101  
 Percent Similarity: 62.90% Conservative: 55  
 Best Local Similarity: 40.73% Mismatches: 79  
 Query Match: 37.70% Indels: 13  
 DB: 19 Gaps: 5  
 US-09-955-526-4 (1-248) x AAV59067 (1-2634)  
 QY 3 GlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyrAspSer 22  
 Db 67 GGNACCATGACATATTTCAT-----CGAAGATCACTTTGATGCGS 108  
 QY 23 LeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyrLeu 42  
 Db 109 CTTTAAATTTTCTCATATACCCCGTCAACCGCAGCAGCAGCAGGAGGTCTATGCA 168  
 QY 43 ThrLeuLysCysAlaValAlaSerAlaGlyAlaValTyrLeuHisIleLeuTrpAsn 62  
 Db 169 AGTTTGGCTTGTATGTTTGGCGCTGCGCTGGCTCCCTGATATGTTGGCTGATG 228  
 QY 63 Ile-----GlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80  
 Db 229 TTCATTGAGCTGGCTGCTGCTGCTGGCTCCCTGATATGTTGGCTGATG 288  
 QY 81 SerAlaProProTyrGln-----GluGlnLysArgValAlaLeuLeuMetAlaAla 98  
 Db 289 GCAACACCTCATAGCCATGAAACTGACAGAAACAACTGGGACTCTTCTGCTGATTTGCA 348  
 QY 99 LeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSer 118  
 Db 349 TTCCTTACAGGAATTGGCTGGCCCTGCTGGCTGGAGTTTGTATTGCTGTACACCCAGC 408  
 QY 119 IleValPheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaAla 138  
 Db 409 ATCCTTCCCACTGCTTTTCATGGCGCAGCGCAATGATCTTTACCTGCTTCACTCAGTGCA 468  
 QY 139 MetLeuAlaArgArgGluTyrLeuTyrLeuGlyLeuLeuSerSerGlyValSer 158  
 Db 469 CTCATGCCAGGCGCGTAGTACCTCTTCTGGAGGTATCTTGTATGTCAGCCCTGAGC 528  
 QY 159 LeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLys 178  
 Db 529 TTGTTGCTT---TTGCTCCCTGGGGAATGTTTCTTGGATCCATTGGCTTTCCAG 585  
 QY 179 PheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGlu 198  
 Db 586 GCAAACTGTATGTGGACTGGTGGTCAATGTCATGTGTGCTTCTGCTCTTGTATCACTC 645  
 QY 199 IleIleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPhe 218  
 Db 646 ATTATTGAAAAGGCCGCAACATGGAGATCAAGATTATATCTGGCAGCTGCATTGATCTCTC 705  
 QY 219 ThrAspPheGlyAlaValPheValArgIleLeuIleMetLeuLysAsnAlaSerGlu 238  
 Db 706 TTAGATTTCATTACTCTCTCAGAAACATCATGATGATCTGCGCATGAT-----GAA 759  
 QY 239 LysGluGluLysLysLysArg 246  
 Db 760 AAGGATAAAGAAGAAGAAGAA 783

## RESULT 10

ABK84658  
ID ABK84658 standard; cDNA; 2600 BP.

AC  
XX ABK84658;

DT 14-AUG-2002 (first entry)

DE Human cDNA differentially expressed in granulocytic cells #1229.

KW Human; ss; granulocytic cell; DNA chip; bacterial infection;  
KW viral infection; parasitic infection; protozoal infection;  
KW fungal infection; sterile inflammatory disease; psoriasis;  
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;  
KW adult respiratory distress syndrome; inflammatory bowel disease;  
KW Crohn's disease; ulcerative colitis; periodontal disease;  
KW granulocyte activation; chronic inflammation; allergy.

OS Homo sapiens.

PN W0200228999-A2.

XX 11-APR-2002.

XX 03-OCT-2001; 2001WO-US30821.

XX 03-OCT-2000; 2000US-237189P.

XX (GENE-) GENE LOGIC INC.

PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;  
XX WPI; 2002-435328/46.

PT Detecting granulocyte activation by detecting differential expression  
PT of genes associated with granulocyte activation, which serves as  
PT diagnostic markers that is useful for monitoring disease states and  
PT drug toxicity -

XX Claim 1; SEQ ID NO 1229; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation  
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by  
CC DNA chip analysis as given in the specification, and comparing  
CC the expression level to an expression level in an unactivated  
CC GC, where differential expression of Gs is indicative of GCA.  
CC Also included are modulating (M2) GA by contacting GC with an agent  
CC that alters the expression of at least one gene in Gs; (2) screening (M3)  
CC for an agent capable of modulating GCA or an inflammation (especially  
CC chronic) in a tissue, an allergic response in a subject, exposure of a  
CC subject to a pathogen or sterile inflammatory disease using the  
CC gene expression profile; (3) detecting (M4) an inflammation (especially  
CC chronic) in a tissue, an allergic response in a subject, exposure of a  
CC subject to a pathogen or sterile inflammatory disease, by detecting the  
CC level of expression in a sample of the tissue of gene(s) from Gs, where  
CC the level of expression of the gene is indicative of inflammation;  
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,  
CC or allergic response in a subject, exposure of a subject to a pathogen  
CC or sterile inflammatory disease, by contacting a tissue having  
CC inflammation with an agent that modulates the expression of gene(s)  
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for  
CC modulating GA; M3 is useful for screening an agent capable of modulating  
CC GCA preferably in an inflammation in a tissue; M4 is useful for  
CC detecting an inflammation (especially chronic) in a tissue, an allergic  
CC response in a subject, exposure of a subject to a pathogen or sterile  
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,  
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal  
CC reperfusion injury, ARDS, adult respiratory distress syndrome,  
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
CC periodontal disease; also bacterial infection, viral infection,  
CC parasitic infection, protozoal infection, fungal infection and M5 is

CC useful for treating one of the above conditions. The present  
CC sequence represents a gene differentially expressed in granulocytes.  
CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 2600 BP; 619 A; 621 C; 590 G; 770 T; 0 other;

## Alignment Scores:

Pred. No.: 1.54e-45 Length: 2600  
Score: 473.50 Matches: 101  
Percent Similarity: 62.10% Conservative: 53  
Best Local Similarity: 40.73% Mismatches: 81  
Query Match: 37.22% Indels: 13  
DB: 24 Gaps: 5

US-09-955-526-4 (1-248) x ABK84658 (1-2600)

QY 3 GlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyrAspSer 22  
DB 35 GGAACCATGAACATATTTGAT-----CGAAGATCACTTTGATGCG 76  
QY 23 LeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyrLeu 42  
DB 77 CTTTAAATTTCTCATATAACCCCGTCAACGAGCAGCACCTGAAGAAGGTCTATGCA 136  
QY 43 ThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrpAsn 62  
DB 137 AGTTTGGCCCTTTGATGTTTGTGGCGCTGCGAGGGCCCTATGTCATATGGTCACTCAT 196  
QY 63 Ile-----GlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80  
DB 197 TTCATTGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 256  
QY 81 SerAlaProProTyrGln-----GluGlnLysArgValAlaLeuLeuMetAlaAlaAla 98  
DB 257 GCAACACCTCATAGCCATGAACCTGAACAGAAAGACTGGGACTTCTTGTGGATTGCA 316  
QY 99 LeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSer 118  
DB 317 TTCCTTACAGGAGTTGGCTGGCCCTGGAGTTTGTATTGTGTCTCAACCCCGCAGC 376  
QY 119 IleValPheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaAla 138  
DB 377 ATCCTTCCCCTGCTTCATGCGGCACAGCAATGATCTTTACCTGCTTCAACCTCAGTGCA 436  
QY 139 MetLeuAlaArgArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSer 158  
DB 437 CTCATATGCCAGGCGCGTAGCTACCTCTTTCTGGAGGATATCTGTATGTGAGCCCTGAGC 496  
QY 159 LeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLys 178  
DB 497 TTGTGCTT---TTGCTTCCCTGGGAAATGTTTCTTTGGATCCCAITTTGGCTTCCAG 553  
QY 179 PheGluLeuTyrPheGlyLeuValPheValGlyTyrIleValPheAspThrGlnGlu 198  
DB 554 GCAACACCTGATGTGGGACTGGTGGTTCATGTGTGGCTGCTGCTGCTGCTGCTGCTGCT 613  
QY 199 IleIleGluLysAlaHisLeuGlyAspMetAspTyrValIlyshHisAlaLeuThrLeuPhe 218  
DB 614 ATTATTGAAAGGCCGCAACATGGAGATCAAGATTATATCTGGCATTCGATTCCTCTTC 673  
QY 219 ThrAspPheGlyAlaValPheValArgIleIleIleMetLeuLysAsnAlaSerGlu 238  
DB 674 TTGATTTCAATTACTGCTTCACAAAACCTCATGATGATGCTGCTGCTGCTGCTGCTGCT 727  
QY 239 LysGluGluLysLysLysLysArg 246  
DB 728 AAGGATAAGAAGAAAGAGAGAA 751

RESULT 11  
ABX19768





of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 751 BP; 163 A; 177 C; 185 G; 225 T; 1 other;

## Alignment Scores:

Pred. No.: 1,55e-35 Length: 751  
Score: 382.50 Matches: 87  
Percent Similarity: 59.36% Conservative: 43  
Best Local Similarity: 39.73% Mismatches: 78  
Query Match: 30.07% Indels: 12  
DB: 24 Gaps: 4

US-09-955-526-4 (1-248) x ABQ56073 (1-751)

QY 3 GlyPheThrSerPheAspSerGlnSerAlaSerArgAsnArgTrpSerTyAspSer 22  
Db 60 GGAACCATGACATATTGAT-----CGAAGATCAACITGATGCG 101  
QY 23 LeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyLeu 42  
Db 102 CTTTAAATTTCTCATATAACCCGTCACGACGACGACCCGTAAGAAGGCTATGCA 161  
QY 43 ThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyLeuHisIleLeuTrpAsn 62  
Db 162 AGTTTGCCCTTGATGTTGTGGCGCTGCGAGGCGCTATGTCATATGGFCACCTCAT 221  
QY 63 Ile-----GlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80  
Db 222 TTCATTACGGCTGGCGTGTGCTGCTGGGCTCCCTGATATGATGATTGGCTGATG 281  
QY 81 SerAlaProProTyrgln-----GluGlnLysArgValAlaLeuLeuMetAlaAla 98  
Db 282 GCAACACCTCFATAGCCATGAAACTGAACAGAAAGACTGGGACTTCTGCTGGATTGCA 341  
QY 99 LeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSer 118  
Db 342 TTCTTTACAGGAGTTGGCTGGCCCTGCCCTGGAGTTGTTGATTCGTCTACACCCAGC 401  
QY 119 IleValPheGlyAlaPheValGlyCysAlaValAlaPheGlyCysPheSerAlaAla 138  
Db 402 ATCCCTTCCCACTGCTTTCATGGCGACGCAATGATCTTTACCTGCTTACCCCTCAGTGCA 461  
QY 139 MetLeuAlaArgArgGluTyLeuTyLeuTyLeuGlyLeuLeuSerSerGlyValSer 158  
Db 462 CTCATGCCAGGCGCGTAGTACCTCTTCTGGGAGGTATCTGTATGTCACGCCCTGAG 521  
QY 159 LeuLeuPheTrpLeuHisPheAlaSerIlePheGlyGlySerMetAlaValPheLys 178  
Db 522 CTGTGGTCTTTGCTTCCCTGGGAAAGTTTCTTT---GGATCCATTGGCTTTCAG 578

QY 179 PheGluLeuTyrrPheGlyLeuLeuValPheValGlyTyrrIleValPheAspThrGlnGlu 198  
Db 579 GCAAACTGATATWGGAGCTGGTGCAATGTGGCTTGGC-CTTTTGTACTCACTC 637  
QY 199 IleIleGluLysAlaHisLeuGlyAspMetAspTyrrValIysHisAlaLeuThrLeu 217  
Db 638 ATTATTGAAGGCCCGAACATGGAGATCAAGATTATATCTGGCACATGATGATCTC 694

## RESULT 13

ABV88094/C  
ID ABV88094 standard; cDNA; 536 BP.

XX AC ABV88094;

XX DT 13-DEC-2002 (first entry)

XX DE Human colon cancer related cDNA SEQ ID NO 1405.

XX KW Human; colon; cancer; cytostatic; tumour; gene therapy; vaccine; gene;  
XX SS.

XX OS Homo sapiens.

XX PN WO200258534-A2.

XX PD 01-AUG-2002.

XX PF 19-NOV-2001; 2001WO-US43704.

XX PR 20-NOV-2000; 2000US-252222P.

XX PR 06-FEB-2001; 2001US-267011P.

XX PR 28-MAR-2001; 2001US-279670P.

XX PR 10-JUL-2001; 2001US-304037P.

XX PA (CORI-) CORIXA CORP.

XX PI Stolk JA, Xu J, Chenault RA, Meagher MJ, Secrist H, King GE;

XX DR WPI; 2002-608400/65.

XX PT New isolated tumor colon polynucleotide and polypeptide, useful for the  
diagnosis, prevention and/or treatment of cancer, in particular colon  
cancer -

XX PS Claim 1; SEQ ID NO 1405; 266pp + Sequence Listing; English.

XX CC The invention relates to a human colon tumour expressed polynucleotide  
(I) encoding a polypeptide (II, ABP67991-ABP67996) comprising: (i) any of  
2600 fully defined nucleotide sequences (ABV8669-ABV89289); (ii)  
complements of (i); (iii) at least 20 contiguous residues of (i); (iv)  
sequences that hybridize to (i), under moderately stringent conditions;  
(v) sequences having at least 75% or 90% identity to (i); or (vi)  
degenerate variants of (i). The compositions and methods of the present  
invention are useful for the diagnosis, prevention and/or treatment of  
cancer, particularly colon cancer. (I) can be used in gene therapy and  
(I) and (II) are useful in pharmaceutical compositions such as vaccines.  
CC Note: The sequence data for this patent did not form part of the printed  
specification, but was obtained in electronic format directly from WIPO  
at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 536 BP; 176 A; 122 C; 133 G; 105 T; 0 other;

## Alignment Scores:

Pred. No.: 1,91e-34 Length: 536  
Score: 371.50 Matches: 76  
Percent Similarity: 65.88% Conservative: 36  
Best Local Similarity: 44.71% Mismatches: 55  
Query Match: 29.21% Indels: 3  
DB: 24 Gaps: 2

US-09-955-526-4 (1-248) x ABV88094 (1-536)

QY 65 GlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeuSerAlaProPro 84



ID ABV25317 standard; cDNA; 638 BP.  
 XX AC ABV25317;  
 XX DT 16-SEP-2002 (first entry)  
 XX DE Human prostate expression marker cDNA 25308.  
 XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW KW pharmacogenomic marker; gene; ss.  
 XX OS Homo sapiens.  
 XX PN WO200160860-A2.  
 XX PD 23-AUG-2001.  
 XX PF 20-FEB-2001; 2001WO-US05171.  
 XX PR 17-FEB-2000; 2000US-183319P.  
 PR 16-MAR-2000; 2000US-189862P.  
 PR 25-MAY-2000; 2000US-207454P.  
 PR 05-JUN-2000; 2000US-211314P.  
 PR 18-JUL-2000; 2000US-219007P.  
 PR 13-DEC-2000; 2000US-255281P.  
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX PI Schlegel R, Endege WO, Monahan JE;  
 XX DR WPI; 2001-662795/76.  
 XX PT Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful  
 PT for detecting presence of prostate cancer, stage of prostate cancer  
 XX Claim 1; Page 4984; 11750pp; English.  
 XX The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (I) is useful for:  
 CC (a) assessing whether a patient is afflicted with prostate cancer;  
 CC (b) monitoring the progression of prostate cancer in a patient;  
 CC (c) assessing the efficacy of a test compound to inhibit prostate  
 CC cancer in a patient;  
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
 CC in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound;  
 CC (g) determining whether prostate cancer has metastasized in a patient;  
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
 CC patient;  
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.  
 XX Sequence 638 BP; 129 A; 155 C; 163 G; 191 T; 0 other;  
 SQ

Alignment Scores:  
 Pred. No.: 4.2e-27 Length: 638  
 Score: 310.50 Matches: 68  
 Percent Similarity: 56.50% Conservative: 45  
 Best Local Similarity: 34.00% Mismatches: 62  
 Query Match: 24.41% Indels: 25  
 DB: 23 Gaps: 4  
 US-09-955-526-4 (1-248) x ABV25317 (1-638)  
 QY 3 GlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyrAspSer 22  
 Db 89 GGAACCATGACATATTTGAT-----CGAAGATCAACTTTGATGCG 130  
 QY 23 LeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyrLeu 42  
 Db 131 CTTTAAATTTCTCATATATACCCGTCACGACGACCACTGAAGAGGCTATGCA 190

Search completed: September 22, 2003, 15:34:05  
 Job time : 273 secs

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	688.5	54.1	884	4	US-09-325-932A-43	Sequence 43, Appl
2	499.5	39.3	527	4	US-09-325-932A-44	Sequence 44, Appl
3	479.5	37.7	2634	2	US-08-818-514-1	Sequence 1, Appl
C	479.5	37.7	2634	2	US-08-818-514-2	Sequence 2, Appl
4	479.5	37.7	2634	3	US-09-115-934A-1	Sequence 1, Appl
5	479.5	37.7	2634	3	US-09-115-934A-2	Sequence 2, Appl
C	479.5	37.7	2634	4	US-09-611-175-1	Sequence 1, Appl
6	479.5	37.7	2634	4	US-09-611-175-2	Sequence 2, Appl
7	479.5	37.7	2634	3	US-09-385-983-231	Sequence 231, App
8	188	14.8	601	3	US-09-362-123A-1	Sequence 1, Appl
9	165	13.0	1316	4	US-09-149-476-184	Sequence 184, App
10	165	13.0	1596	4	US-09-996-243-1	Sequence 1, Appl
11	165	13.0	1943	4	US-09-996-243-1	Sequence 1, Appl
12	165	13.0	1943	4	US-09-996-243-1	Sequence 1, Appl

Db	62	CTTCTGTTGAATATTGGAGGCTCCTCAGCGGGCTCGCTTCGATTCGTTGGTTCGTAAATCGG	121
Qy	79	LeuLeuSerAlaPro-----ProTyrGlnGluGlnTysArgValAlaLeuLeuMetAla	96
Db	122	CTCTTATCCGTCCTACTTCTCTCGAAACAATCAGGCTAAGAGAGCTGCCTGCTCTCGCA	181
Qy	97	AlaAlaLeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAsp	116
Db	182	GCTCTCGGTTCAAGGAGCTACTCTGGACCGCTATCGACGGGCTCATTAATATTGAC	241
Qy	117	ProSerIleValPheGlyAlaPheValcIysAlaValAlaValPheGlyCysPheSerAla	136
Db	242	TCCAGTATACTGGTGAGTGGCTTTGTTGGGACCTCTTTGGCCTTCGCTGCTTTTCGGCA	301
Qy	137	AlaAlaMetLeuAlaAaArgArgGluTyrIleuTyrLeuGlyGlyLeuLeuSerSerGly	156
Db	302	GCACGATACAGCCAGGAGACGGGAATACCTATTTTGGGAGGAATATTGGGCTCGGGA	361
Qy	157	ValSerLeuLeuPheTyrLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaVal	176
Db	362	ATCAGCATATTGATGTGGCTGCACTAGCATCTCGATTTTGGTGGTTCCTTCGCGCAT	421
Qy	177	PheLysPheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThr	196
Db	422	TACACATTGGAGATCTACTTCGGTCTGCTAGTTTTCCTTGGGTATATTATATTATGACAC	481
Qy	197	GlnGluIleIleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThr	216
Db	482	CAGATGATCATCGAAGACGGGACCATCGAGACTATGATTATTTAAAAACATTCACTGGCA	541
Qy	217	LeuPheThrAspPheGlyAlaValPheValArgIleLeuIleIleuLeuLysAsnAla	236
Db	542	CTCTTCATTCGCTTCGTGTTATTTGTCCTCGATGGTTCATTAATGCAAGAATGCA	601
Qy	237	---SerGluTysGluGluLysLysLysArgArg	247
Db	602	CACAGTAAATCCAGGAAGGGAAGAAAGAAAGGAAGG	637

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RESULT 2
US-09-325-932A-44
; Sequence 44, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 527
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-325-932A-44

Alignment Scores:
Pred. No.: 1.59e-56
Score: 499.50
Percent Similarity: 79.72%
Best local Similarity: 70.63%
Query Match: 39.27%
DB: 4
Matches: 101
Conservative: 13
Mismatch: 26
Indels: 4
Gaps: 1

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US-09-955-526-4 (1-248) x US-09-325-932A-44 (1-527)

QY 1 MetGluGlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyr 20  
|||::: ||| ||| ||| ||| ||| ||| |||  
Db 107 ATGGACGGCTTCGCTCCCTCGCTGCCAGTCG-----AGCGCAAGGGGTGGAGCCAC 157  
  
QY 21 AspSerLeuLysAsnPhaPheArgGlnIleSerProLeuValcIcnThrHisLeuLysGlnVal 40

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Db      158  GATTTCCTCCAGAACTTCGGCAGATATCTCCGCCGCTCCAAATCTCACCTCAGAAATGTT 217
Qy      41  TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisLeu 60
Db      218  TATCTGTCTCTTATGCTGTGCGCTTGATGCTTCGGCCGGTGGTGCTTACCTGCATCTGATG 277
Qy      61  TrpAsnIleGlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
Db      278  CTGCAACATCGCGGGGCTCCTCAGCAAAATGCTTTGTCATCGGAAGCATCGTGTTGGCTGCTT 337
Qy      81  SerAlaProProTyrGlnGluGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100
Db      338  TCGATTCTCTCCACATGAGAGCAAAAGAGGTTTGGTCTGCTCATGCGCGGCGCTCTCTTT 397
Qy      101  GluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleVal 120
Db      398  GAAGGAGCGGTGATCGGTCCTCTCATCGAAGCGGCCATTAAAGTCTGCGCCGAGCATGTG 457
Qy      121  PheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaAlaMetLeu 140
Db      458  ATAAGCGCAATTGTGGGATCTGCGCTGGCCTTGCTTGTTCTCGGGCGCAGC-ATGTTG 516
Qy      141  AlaArgArg 143
Db      517  GCTAGGCGG 525

RESULT 3
US-08-818-514-1
; Sequence 1, Application US/08018514
; Patent No. 5837838
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Xu, Qunli
; TITLE OF INVENTION: BAX Inhibitor Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,514
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2634 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-818-514-1

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Alignment Scores:	
Pred. No.:	8.9e-53
Score:	479.50
Length:	2634
Percent Similarity:	62.90%
Matches:	101
Best Local Similarity:	40.73%
Mismatches:	79
Query Match:	37.70%
Indels:	13
Conservative:	55

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DB: 2 Gaps: 5
US-09-955-526-4 (1-248) x US-08-818-514-1 (1-2634)
QY 3 GlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyrAspSer 22
Db 67 GGAACCATGAACATATTGAT-----CGAAAGATCAACTTTGATGG 108
QY 23 LeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyrLeu 42
Db 109 CTTTAAATTTTCTCATATACCCGTCACGACGACCTGAAGAAGTCTATGCA 168
QY 43 ThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrpAsn 62
Db 169 AGTTTGGCCCTTGTATGTTTGGGGGTGACAGGGCCTATGTCCATATGTCACCTAT 228
QY 63 Ile-----GlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
Db 229 TTCATTACAGGCTGGCGTCTGCTGCTGGGCTCCCTCATATATGATGATTGGCTGATG 288
QY 81 SerAlaProProTyrGln-----GluGlnLysArgValAlaLeuLeuMetAlaAla 98
Db 289 GCAACACCTCATAGCCATGAACCTGAACAGAAACCTGGGACTTCTTCTGGATTTGCA 348
QY 99 LeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSer 118
Db 349 TTCTTACAGGAATTTGGCTGGCCCTGCGCTGGAGTTTGTATGCTGTCAACCCACG 408
QY 119 IleValPheGlyAlaPheValGlyCysAlaValAlaPheGlyCysPheSerAlaAla 138
Db 409 ATCCTTCCCACTGCTTTCATGGGACGCAATGATCTTTACCTGCTTCAACCTCAGTGCA 468
QY 139 MetLeuAlaArgArgGlnTyrLeuTyrLeuGlyLeuLeuSerSerGlyValSer 158
Db 469 CTCATGCGAGCGCGCTAGCTACCTCTTCTGGAGGATCTGTGATGTCAGCCCTGAGC 528
QY 159 LeuLeuPheTrpLeuHisPheAlaSerIlePheGlyGlySerMetAlaValPheLys 178
Db 529 TTGTTGCTT--TTGCTTCCCTGGGAATGTTTCTTTGGATTCATTTGGCTTTCCAG 585
QY 179 PheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGlu 198
Db 586 GCAACACCTCATGCGGACTGTGGTCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 645
QY 199 IleIleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPhe 218
Db 646 ATATTTGAAGCCGCAACATGGAGATCAAGATATATATCTGGCAGTCGATGATCTCTC 705
QY 219 ThrAspPheGlyAlaValPheValArgIleLeuIleMetLeuLysAsnAlaSerGlu 238
Db 706 TTAGATTTCATTACTCTCTCAGAAACCTCATGATCATCTGSCCATGAAT-----GAA 759
QY 239 LysGluGluLysLysLysArg 246
Db 760 AAGGATAGAGAAAGAGAGAGAA 783
RESULT 4
US-08-818-514-2/c
; Sequence 2, Application US/08818514
; Patent No. 5837836
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Xu, Qunli
; TITLE OF INVENTION: BAX Inhibitor Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
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QY 199 IleIleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPhe 218
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1989 ATTATTGAAGGCGCAACATGAGATATATCTGGCACTGCATTGATCTCTTC 1930

QY 219 ThrAspPheGlyAlaValPheValArgIleLeuIleLeuMetLeuLysAsnAlaSerGlu 238
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1929 TTAGATTTCATTACTGCTCTCAGAAACTCATGATGATCTCTGGCCATGAAT-----GAA 1876

QY 239 LysGluGluLysLysLysArg 246
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1875 AAGGATAGAGAAAGAGAGAGAA 1852

RESULT 5
US-09-115-934A-1
; Sequence 1, Application US/09115934A
; Patent No. 6130317
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: BAX Inhibitor Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/115,934A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/818,514
; FILING DATE: 14-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2634 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-115-934A-1

Alignment Scores:
Pred. No.: 8.9e-53 Length: 2634
Score: 479.50 Matches: 101
Percent Similarity: 62.90% Conservative: 55
Best Local Similarity: 40.73% Mismatches: 79
Query Match: 37.70% Indels: 13
DB: 3 Gaps: 5

US-09-955-526-4 (1-248) x US-09-115-934A-1 (1-2634)

QY 3 GlyPheThrSerPheAspSerGlnSerAlaSerArgAsnArgTrpSerTyrAspSer 22
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 67 GGAACCATGACATATTGAT-----CGAAGATCACTTTGATGCG 108

QY 23 LeuLysAsnPheArgGlnIleSerProLeuValGlnThrLeuLysGlnValTyrLeu 42
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 109 CTTTAAATTTCTCATATAACCCGCTCAACGACAGCAGCCTGAAGAGGTCATGCA 168

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QY 43 ThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrpAsn 62
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 169 AGTTTGGCCCTTGTATGTTTGTGGCGCTGCAGGGCCCTATGTCCATATGGTGCACAT 228

QY 63 Ile-----GlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 229 TTCAATCAGGCTGGCCCTGCTGCTGCTGGCTCCCTGATATGATGATTTGGCTGATG 288

QY 81 SerAlaProProTyrGln-----GluGlnLysArgValAlaLeuLeuMetAlaAla 98
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 289 GCAACACCTCATAGCCATGAACCTGAACAGAGAAAAAAGTGGGACTTCTGCTGGATTGCA 348

QY 99 LeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSer 118
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 349 TTCCTTACAGGAATGGCCCTGGCCCTGCTGGAGTTTGTATTTGCTGTCAACCCGAGC 408

QY 119 IleValPheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAla 138
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 409 ATCCTTCCCACTGCTTTCATGGCAGCGCAATGATCTTACCTGCTTCAACCTCAGTGCA 468

QY 139 MetLeuAlaArgArgGluTyrLeuTyrLeuGlyLeuLeuSerSerGlyValSer 158
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 469 CTCATGCGAGCGCGCTAGCTACCTCTTCTGGAGGTATCTTGTGATGACCCCTGAGC 528

QY 159 LeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLys 178
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 529 TTGTTGCTT---TTGCTTCCCTGGGGAATGTTTCTTTGGATCCATTGGCTTTCCAG 585

QY 179 PheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGln 198
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 586 GCAAACTGTATGTGGACTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 645

QY 199 IleIleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeu 218
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 646 ATTATTGAAGGCGCAACATGAGATCAAGATATATCTGCGACTGCATGATCTGCTC 705

QY 219 ThrAspPheGlyAlaValPheValArgIleLeuIleLeuMetLeuLysAsnAlaSerGlu 238
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 706 TTAGATTTCATTACTGCTCTCAGAAACTCATGATGATCTCTGCGCCATGAAT-----GAA 759

QY 239 LysGluGluLysLysLysArg 246
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 760 AAGGATAGAGAAAGAGAGAGAA 783

RESULT 6
US-09-115-934A-2/c
; Sequence 2, Application US/09115934A
; Patent No. 6130317
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Xu, Qunli
; TITLE OF INVENTION: BAX Inhibitor Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/115,934A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/818,514
; FILING DATE: 14-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2634 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-115-934A-1

```



```

; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2634 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-115-934A-2

Alignment Scores:
Pred. No.: 8.9e-53 Length: 2634
Score: 479.50 Matches: 101
Percent Similarity: 62.90% Conservative: 55
Best Local Similarity: 40.73% Mismatches: 79
Query Match: 37.70% Indels: 13
DB: 3 Gaps: 5

US-09-955-526-4 (1-248) x US-09-115-934A-2 (1-2634)
QY 3 GlyPheThrSerPhePheaspSerGlnSerAlaSerArgAsnArgTrpSerTyrAspSer 22
Db 2568 GSAACCATGACATATTTGAT-----CGAAGATCAACTTTGATGCG 2527
QY 23 LeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyrLeu 42
Db 2526 CTTTAAATTTCTCATATACCCGTCACGCAGCAGCCTGAAAGAGGCTATGCA 2467
QY 43 ThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrpAsn 62
Db 2466 AGTTTGGCCTTTGTATGTTGTGGCGCTGCGAGGCGCTATGCTCATATGCTCACTCAT 2407
QY 63 Ile-----GlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
Db 2406 TTCATTCAGCTGGCTGCTGCTGCTGGCTGGCTGCTGATATGATGTTGGCTGATG 2347
QY 81 SerAlaProProTyrGln-----GluGlnLysArgValAlaLeuLeuMetAlaAla 98
Db 2346 GCACACCTCATAGCATGAACTGACACGACGACGACGACGACGACGACGACGACGACG 2287
QY 99 LeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSer 118
Db 2286 TTCCTTACAGGAATGGCCTGGCCTGGCCTGGCCTGGCCTGGCCTGGCCTGGCCTGGC 2227
QY 119 IleValPheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaAla 138
Db 2226 ATCCTTCCCACTGCTTTCATGAGGACGACGACGACGACGACGACGACGACGACGACG 2167
QY 139 MetLeuAlaArgArgGlyTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSer 158
Db 2166 CTCATGCGCAGGCGCGTAGCTACCTCTTCTGGAGGATCTGTATGTCAGCCCTGAGC 2107
QY 159 LeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLys 178
Db 2106 TTGTTGCTT---TTGCTTCCCTGGGGAATGTTTCTTGGATCCCACTTTGGCTTTCCAG 2050
QY 179 PheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGlu 198
Db 2049 GCAACCTGATGTGGAGCTGGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1990
QY 199 IleIleGluLysAlaHisLeuGlyAspMetAspTyrValIysHisAlaLeuThrLeuPhe 218
Db 1989 ATTATTGAAAGCCGCAACATGAGATCAAGATATATCTGGCACTGCTGCTGCTGCTGCT 1930
QY 219 ThrAspPheGlyAlaValPheValArgIleLeuIleMetLeuLysAsnAlaSerGlu 238
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QY 239 LysGluGluLysLysLysArg 246

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Db 1875 AAGGATAAGAAAGAAAGAAAGAA 1852
RESULT 7
US-09-611-175-1
; Sequence 1, Application US/09611175
; Patent No. 6545128
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: BAX Inhibitor Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/611,175
; FILING DATE: 06-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/115,934
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/818,514
; FILING DATE: 14-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2634 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-611-175-1

Alignment Scores:
Pred. No.: 8.9e-53 Length: 2634
Score: 479.50 Matches: 101
Percent Similarity: 62.90% Conservative: 55
Best Local Similarity: 40.73% Mismatches: 79
Query Match: 37.70% Indels: 13
DB: 4 Gaps: 5

US-09-955-526-4 (1-248) x US-09-611-175-1 (1-2634)
QY 3 GlyPheThrSerPhePheaspSerGlnSerAlaSerArgAsnArgTrpSerTyrAspSer 22
Db 67 GAACCATGACATATTTGAT-----CGAAGATCAACTTTGATGCG 108
QY 23 LeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyrLeu 42
Db 109 CTTTAAATTTCTCATATACCCGTCACGCAGCAGCCTGAAAGAGGCTATGCA 168
QY 43 ThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrpAsn 62
Db 169 AGTTTGGCCTTTGTATGTTGTGGCGCTGCGAGGCGCTATGCTCATATGCTCACTCAT 228
QY 63 Ile-----GlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80

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229	DB	TTCATTCAGGCTGGCGTGTCTCTGCTCTGGCTCTCCCTGATATTGATGATTGGCGTGATG	288
81	QY	SerAlaProProTyrGln-----GluGlnLysArgValAlaLeuLeuMetAlaAla	98
289	DB	GCACACCTCATGACCATGAACTGAACACAAAAAACTGGGAGTTCTTCTGCTGGATTGCA	348
99	QY	LeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAlaPheAspProSer	118
349	DB	TTCCCTTACAGAAATTGGCTCTGGGCGCTGGCCCTGGAGTTTGTATTGCTCTCAACCCAGC	408
119	QY	IleValPheGlyAlaPheValCylCysAlaValValPheGlyCysPheSerAlaAlaAla	138
409	DB	ATCCTTCCCAGTCTTTCATGGCAGCGCATGATCTTTACCTGCTTCCCTCAGTGCA	468
139	QY	MetLeuAlaArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSer	158
469	DB	CTCTATGCGAGCGCGCTAGCTACCTCTTCTGGGAGGTATCTTGATGTCAGCCCTGAGC	528
159	QY	LeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLys	178
529	DB	TGTTTGCTT---TGCTCTCCCTGGGAAGTTCCTTGGATCCATTTGGCTTTTCCAG	585
179	QY	PheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGlu	198
586	DB	GCAAACTGTATGTGGGACTGGTGTCTATGTCGTGCTCTCTTGGATCCATTTGATACCTCAACTC	645
199	QY	IleIleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPhe	218
646	DB	ATTATTGAAGAGCGCGAATCATGGAGATCAAGATTATATCTGGCAGCTCATGTATCTCTTC	705
219	QY	ThrAspPheGlyAlaValPheValArgIleLeuIleMetLeuLysAsnAlaSerGlu	238
706	DB	TTAGATTTTCATTACTGCTCTTCAGAAAACTCATGATGATCCTGGCCATGAAT-----GAA	759
239	QY	LysGluGluLysLysLysLysArg	246
760	DB	RAGGATAAGAGAAAGAGAAGAAA	783

RESULT 8

US-09-611-175-2/c

; Sequence 2, Application US/09611175

; Patent No. 6545128

; GENERAL INFORMATION:

; APPLICANT: Reed, John C.

; Xu, Qunli

; TITLE OF INVENTION: BAX Inhibitor Proteins

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESS: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; Zip: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/611,175

; FILING DATE: 06-Jul-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/115,934

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/818,514

; FILING DATE: 14-MAR-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-LJ 3209

; TELECOMMUNICATION INFORMATION:

Db 542 TTGTGCTTTCCTCTCGGGAATGTTTCTTTGGATCCATTGGCTTTTCAGC 592

RESULT 10  
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 ; Sequence 1, Application US/09362123A  
 ; Patent No. 6451558  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cooke, Michael Paul  
 ; APPLICANT: Holness, Claire  
 ; APPLICANT: Sirenko, Oksana  
 ; TITLE OF INVENTION: No. 6451558el Genes in the Control of Hematopoiesis  
 ; FILE REFERENCE: 4-30629A/SYS  
 ; CURRENT APPLICATION NUMBER: US/09/362.123A  
 ; CURRENT FILING DATE: 1999-07-27  
 ; PRIOR APPLICATION NUMBER: 09/128,310  
 ; PRIOR FILING DATE: 1998-08-03  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 1316  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-362-123A-1

Alignment Scores:  
 Pred. No.: 8.52e-12 Length: 1316  
 Score: 165.00 Matches: 61  
 Percent Similarity: 46.55% Conservative: 47  
 Best Local Similarity: 26.29% Mismatches: 86  
 Query Match: 12.97% Indels: 38  
 Db: 4 Gaps: 11

US-09-955-526-4 (1-248) x US-09-362-123A-1 (1-1316)

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Db	483	ATCAGCAGAACGCCCTGTCTCATGATCAACTCATGATGAGAGGCTCTTGGGTGACAAATGGT	542
Qy	69	--ThrMetAlaCysMetGlySerMetValTirPLeuLeuSerAlaProProTyrGlnGlu	87
Db	543	GTGACCTTTGGAGCCATCGTTGGAGCTGGAATGCTGGTACGATCAATACCATATGACCAG	602
Qy	88	Gln-----LysArgValAlaLeuLeuMetAlaAlaLeuPheGluGlyAlaSer	104
Db	603	AGCCAGGCGCCAAAGCATCTTCTGTTGGTTGCTACATCTTGGTGTGATG---GGTGCAATG	659
Qy	105	IleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleValPheGlyAlaPhe	124
Db	660	GTGGCTCTCTGACAAATATATAGG-----GGTCTCTTCTCATCAGAGCTGCATGG	710
Qy	125	ValGlyCysAlaValValPheGlyCysPheSerAlaAlaAlaMetLeuAlaArgArgArg	144
Db	711	TACACAGCTGGCAATTTG--GGAGGCTCTCCACTGTGCCCATGTGCGCCCATGAA	767
Qy	145	GluTyrLeuTyrLeuGlyClyLeuLeuSerSerGlyValSerLeuLeuPheTirPleuHis	164
Db	768	AAGTTTCTTGAACATGGGTGCACCCCTGGGAGTGGGCTGGGTCTGGTC-----	815
Qy	165	PheAlaSerSerIlePheGlyGlySerMet-----GlyGlyGlyGlyGlyGlyGlyGly	174
Db	816	TTTGTGCTCTCATG-----GGAICTATGTTTCTTCCACCTACCACCGTGGCTGGTGGC	869
Qy	175	AlaValPheLysPheLeuLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPhe	194
Db	870	ACTCTTTACTAGTGGCAATGTACGGTGGATAGTTCITTTTTCAGCATGTTCTCTCTGAT	929
Qy	195	AspThrGlnGluIleIleGluLysAlaHisLeuGlyAspMet-----GlyGlyGlyGly	208
Db	930	GATACCCAGAAATATCAAGGTCGACGAAGTATACCAATGTATGGATGTCAAAATAT	967



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; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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## Alignment Scores:

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Pred. No.: 1.16e-11
Score: 165.00
Percent Similarity: 46.55%
Best Local Similarity: 26.29%
Query Match: 12.97%
DB: 4
Length: 1596
Matches: 61
Conservative: 47
Mismatches: 86
Indels: 38
Gaps: 11

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US-09-955-526-4 (1-248) x US-09-149-476-184 (1-1596)
QY 36 HisLeuLysGlnValTyrLeuThrLeuCysAlaLeuValAlaSerAlaAlaGlyAla 55
Db 503 CATTCACCTATATGACTTACGAGGAGATTTGGTTTACAGCTTTGCTGCATAGCA 562
QY 56 TyrLeuHis-----lleLeuTrpAsnIle-----GlyGlyLeuLeuThr 68
Db 563 ATCAGCAGAGAGCGCTGTTCTCATGAAGCTTCATCATGAGAGGCTTTGGTGACAATTGGT 622
QY 69 ---ThrMetAlaCysMetGlySerMetValTrpLeuLeuSerAlaProTyrGlnGlu 87
Db 623 GTGACCTTTGCAGCCATGTTGGAGCTGGAATCTGCTAGCATCAATACCATATGACCG 682
QY 88 Glu-----LysArgValAlaLeuMetAlaAlaAlaLeuPheGluGlyAlaSer 104
Db 683 AGCCAGGCGCCAAAGCATCTTGTGTTGCTACATCTGCTGGTGTGATG---GGTGCAGTG 739
QY 105 IleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleValPheGlyAlaPhe 124
Db 740 GTGGCTCCTCTGACAAATATTAGGG-----GGTCTCTTCTCATCAGAGCTGCAITGG 790
QY 125 ValGlyCysAlaValValPheGlyCysPheSerAlaAlaAlaMetLeuAlaArgArg 144
Db 791 TACACAGCTGGCATTTGTG---GGAGCGCTCTCCACTGTGGCCAGTGTGGCCCGAGTAA 847
QY 145 GluTyrLeuTyrLeuGlyLeuLeuSerSerGlyValSerLeuLeuPheTrpLeuHis 164
Db 848 AAGTTTCTGAACATGGGTGCACCCCTGGGAGTGGGCTGGGCTCGTC----- 895
QY 165 PheAlaSerSerIlePheGlyGlySerMet----- 174
Db 896 TTTGTGTCTCTCATTTG-----GGATCTATCTTTTCCACCTACCACCGTGGTGTGCC 949
QY 175 AlaValPheLysPheGluLeuTyrPheGlyLeuValPheValGlyTyrIleValPhe 194
Db 950 ACTCTTTACTCAGTGGCAATGTACGGTGGATTTAGTTCTTTTTCAGCATGTTCCCTTCGTAT 1009
QY 195 AspThrGlnGluIleLeuLysAlaHisLeuGlyAspMet----- 208
Db 1010 GATACCCAGAAAGTAAATCAAGCGTGCAGAGATACCATATGATGAGTTCAAAATAT 1069
QY 209 AspTyrValLysHisAlaLeuThrLeuPheThrAspPheGlyAlaValPheValArgIle 228
Db 1070 GATCCCATTAACCTCGATGCTGAGTATCTACATGATACATATAATATATTTATCGAGTT 1129
QY 229 LeuIleLeuMetLeuLysAsnAlaSerGluLysGlu 240
Db 1130 GCAACTATGCTGCACTGGAGCGCACAGAAAGAAA 1165

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## RESULT 12

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US-09-996-243-1
; Sequence 1, Application US/09996243
; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

```

APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C13  
CURRENT APPLICATION NUMBER: US/09/996,243  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
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PRIOR APPLICATION NUMBER: 60/084600  
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PRIOR APPLICATION NUMBER: 60/087106  
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PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
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/ PRIOR APPLICATION NUMBER: 60/090676
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/ PRIOR APPLICATION NUMBER: 60/091360
/ PRIOR FILING DATE: 1998-07-01
/ PRIOR APPLICATION NUMBER: 60/091478
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/ PRIOR APPLICATION NUMBER: 60/091978
/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/091982
/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 1,58e-11 Length: 1943
Score: 165.00 Matches: 61
Percent Similarity: 46.55% Conservative: 47
Best Local Similarity: 26.29% Mismatches: 86
Query Match: 12.97% Indels: 38
DB: 4 Gaps: 11

US-09-955-526-4 (1-248) x US-09-996-243-1 (1-1943)

QY 36 HisLeuLysGlnValTyrLeuThrLeuCysAlaLeuValAlaSerAlaAlaGlyAla 55
Db CATTCACCTATATGTTACTAGCAGGGAGTATGGTTTACACCTTGTGTCGCATAGCA 511
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QY 88 Gln-----LysArgValAlaLeuLeuMetAlaAlaLeuPheGluGlyAlaSer 104
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QY 105 IleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleValPheGlyAlaPhe 124
Db GTGGCTCTCTGCAATATTAGG-----GGTCCCTCTCTCATGAGCTGATGG 739
QY 125 ValGlyCysAlaValValPheGlyCysPheSerAlaAlaMetLeuAlaArgArg 144
Db TACACAGCTGGCAATTGG---GGAGGCCTCTCCAGCTGGCCCAATGTGGCCCGCATGAA 796
QY 145 GluTyrLeuTyrLeuGlyLeuLeuSerSerGlyValSerLeuLeuPheTrpLeuHis 164
Db AAGTTTCTGAACATGGGTGCACCCCTGGGAGTGGGCTGGTCTCGTC----- 844

165 PheAlaSerSerIlePheGlySerMet----- 174
845 TTTGTGCTCTCATG-----GGAATATGTTTCTCCACCTACACCGTGGCTGTGGCC 898
175 AlaValPheLysPheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPhe 194
899 ACTCTTTACTCAGTGGCAATGACGGTGGATTAGTTCTTTTCAGCATGTTCTCTGTAT 958
195 AspThrGlnGluIleGluLysAlaHisLeuGlyAspMet----- 208
959 GATACCCAGAAAGTAAATCAAGCGTGCAGAGTATCAACATGATGAGGTTCACAAATAT 1018
209 AspTyrValLysHisAlaLeuThrLeuPheThrAspPheGlyAlaValPheValArgIle 228
1019 GATCCCATTAACTCGATGCTGAGTATCTACATGATGATACATTAATATATTATGCGAGT 1078
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1079 GCAACTATGCTGGCAACTGGAGGCAACAGAGAA 1114

RESULT 13
US-09-149-476-308
; Sequence 308, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
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38	EARLIER FILING DATE: 1997-05-23
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44	EARLIER FILING DATE: 1997-04-11
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46	EARLIER FILING DATE: 1997-05-23
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51	EARLIER APPLICATION NUMBER: 60/056,664
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64	EARLIER FILING DATE: 1997-08-22
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77	EARLIER APPLICATION NUMBER: 60/049,610



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; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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QY 56 TyrLeuHis-----IleLeuTrpAsnIle-----GlyGlyLeuLeuThr----- 68
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Db 532 ATCAGCAGAACGCCCTGTTCTCATGAACCTTCATGATCAGAGGCTCTTGGGTGACAATTGGT 591
QY 69 ---ThrMetAlaCysMetGlySerMetValTrpLeuLeuSerAlaProProTyrGlnGlu 87
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Db 592 GTGACCTTTGACGACCATGTTGGAGCTGGAATGCTGGTACGATCAATACCATATGACCAG 651
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Db 979 GATACCCAGAAATATCAAGCGTGCAGAGTATCACCATGTATGAGTTCAAAAATAT 1038
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US-09-313-294A-540
; Sequence 540, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A

; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 540
; LENGTH: 256
; TYPE: DNA
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; OTHER INFORMATION: Incyte ID No. 6476212 700549409H1
US-09-313-294A-540

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; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methano
; Patent No. 6503729
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
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US-08-916-421B-1
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      1638141 ATTGTTGGATTATATCGGAATAGTATTAACTTTGCTTTCATCTTCCAATCTTATCA 1638082
QY      96 AlaAlaAlaLeuPheGluGlyAlaSerIleGly-----Pro 107
      1638081 TTGATTGGATTGCTATTATTGGGGCTATCGTTTGGGCTACTGACCCCTGCTACATTAAATACCA 1638022
QY      108 LeuIle-----GluLeuGlyIleAsnPheAspProSerIleVal 120
      1638021 ATATTCTCAAGCATGGATATTGANCACAGATAGCAATAACCTTAGAAGCAGAGAGTGT 1637962
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      1637961 TTTAACGACCCATTAGGAGTTGTTGTAACACTTATATGTTATCATGCCCTTGGTTTAGCT 1637902
QY      141 AlaArgArgArg-----GluTyr-----LeuTyrLeuGlyGlyLeuLeu----- 153
      1637901 AAAGCTGAGAAATCCAAATCTTGAAATTTTTCATTAGCTGTGGTGGGATAATATTGGGG 1637842
QY      153 ----- 153
DB      1637841 GTTATAGCAGCGAAGTTCTATGAAATTTATTCACAAAAATTAAAGTTTGAGGACTATATT 1637782
QY      154 -----SerSerGlyValSerLeuLeuPheTrpLeuHisPheAlaSerSerIlePhe 170
      1637781 GCTCCATTACTTTAGGATTGGCTATTGCCTTTGG--TATTTGCTGAGGGAATTTTC 1637725
QY      171 -----GlyGlySerMetAlaValPheLysPheGluLeuTyr 182
      1637724 CCATCAATAACTGGCTATGAAATTTAGTGGATTATGGCAGTGGCTATAATGGGATTATAT 1637665
QY      183 PheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluIleIleGluLys 202
      1637664 ATTGGAACGTCATA-----GTGCATAAAAAA 1637638
QY      203 AlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThrAspPheGly 222
      1637637 GAACATAAAAAAGATATGAAAAGGTT-----GCAGTGTATTATGGATCAACATC 1637590
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      1637589 TCCATATTATCAGAAATATTATCTCGTATTATTAGGGGCAAGT 1637545
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus.p2n model

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Title: US-09-955-526-4

Perfect score: 1272

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-TRANS-human40.cdi -LIST=45 -LOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US0955526.cgn1.1.333 -runat\_22092003.151757.12511  
-NCPU=6 -ICPU=3 -NO\_MMAPP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications\_NA:

1: /cgn2.6/ptodata/2/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2.6/ptodata/2/pubpna/PTC\_NEW\_PUB.seq:  
3: /cgn2.6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2.6/ptodata/2/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2.6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:  
6: /cgn2.6/ptodata/2/pubpna/PTCUS\_PUBCOMB.seq:  
7: /cgn2.6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:  
8: /cgn2.6/ptodata/2/pubpna/US08\_PUBCOMB.seq:  
9: /cgn2.6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:  
10: /cgn2.6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:  
11: /cgn2.6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:  
12: /cgn2.6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:  
13: /cgn2.6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:  
14: /cgn2.6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:  
15: /cgn2.6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:  
16: /cgn2.6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:  
17: /cgn2.6/ptodata/2/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1272	100.0	1034	11 US-09-955-526-3 Sequence 3, Appli

2	1027.5	80.8	1009	9	US-09-770-445-223	Sequence 223, Appl
3	988	77.7	735	14	US-10-167-015-15	Sequence 15, Appl
4	963.5	75.1	1218	14	US-10-219-220-232	Sequence 232, Appl
5	955	75.1	989	14	US-10-167-015-17	Sequence 17, Appl
6	884.5	69.5	1026	14	US-10-167-015-31	Sequence 31, Appl
7	879	69.1	1138	14	US-10-167-015-33	Sequence 33, Appl
8	879	69.1	1139	14	US-10-167-015-5	Sequence 5, Appl
9	871	68.5	1026	14	US-10-167-015-3	Sequence 3, Appl
10	786.5	61.8	957	14	US-10-167-015-1	Sequence 1, Appl
11	772.5	60.7	1102	14	US-10-219-220-231	Sequence 231, Appl
12	688.5	54.1	984	14	US-10-219-220-43	Sequence 43, Appl
13	499.5	39.3	527	14	US-10-219-220-44	Sequence 44, Appl
14	491.5	38.6	873	12	US-10-263-828-6	Sequence 6, Appl
15	484.5	38.1	740	14	US-10-167-015-7	Sequence 7, Appl
16	483.5	38.0	2922	9	US-09-925-302-73	Sequence 73, Appl
17	483.5	38.0	2994	13	US-10-044-090-356	Sequence 356, Appl
18	426	33.5	376	10	US-09-878-574-1827	Sequence 1827, Ap
19	422	33.2	308	14	US-10-167-015-22	Sequence 22, Appl
20	371.5	29.2	536	10	US-09-998-598-1405	Sequence 1405, Ap
21	339	26.7	234	14	US-10-167-015-19	Sequence 19, Appl
22	301	23.7	529	12	US-10-002-631C-3	Sequence 3, Appl
23	296	23.3	251	10	US-09-878-574-7224	Sequence 7224, Ap
24	285	22.4	410	10	US-09-960-352-8444	Sequence 8444, Ap
25	280	22.0	803	14	US-10-167-015-21	Sequence 21, Appl
26	255	20.0	257	10	US-09-878-574-6304	Sequence 6304, Ap
27	219	17.2	392	10	US-09-960-352-8713	Sequence 8713, Ap
28	219	17.2	431	10	US-09-960-352-13324	Sequence 13324, A
29	193.5	15.2	250	9	US-09-923-876-298	Sequence 298, App
30	189	14.9	415	11	US-09-918-995-36866	Sequence 36866, A
31	188	14.8	601	11	US-09-871-161-231	Sequence 231, App
32	184	14.5	422	11	US-09-918-995-16385	Sequence 16385, A
33	165	13.0	1316	12	US-10-177-023-1	Sequence 1, Appli
34	165	13.0	1355	11	US-09-822-846-122	Sequence 122, App
35	165	13.0	1394	9	US-09-745-763-67	Sequence 67, Appl
36	165	13.0	1596	11	US-09-809-391-184	Sequence 184, App
37	165	13.0	1943	9	US-09-989-722-1	Sequence 1, Appli
38	165	13.0	1943	9	US-09-989-723-1	Sequence 1, Appli
39	165	13.0	1943	9	US-09-989-279-1	Sequence 1, Appli
40	165	13.0	1943	9	US-09-989-727-1	Sequence 1, Appli
41	165	13.0	1943	10	US-09-989-731-1	Sequence 1, Appli
42	165	13.0	1943	10	US-09-989-732-1	Sequence 1, Appli
43	165	13.0	1943	10	US-09-991-073-1	Sequence 1, Appli
44	165	13.0	1943	10	US-09-990-442-1	Sequence 1, Appli
45	165	13.0	1943	10	US-09-991-163-1	Sequence 1, Appli

#### ALIGNMENTS

RESULT 1  
US-09-955-526-3  
; Sequence 3, Application US/09955526  
; Publication No. US20030009785A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; TITLE OF INVENTION: Plant Cytoprotective Genes and Methods  
; FILE REFERENCE: P-LJ 4868  
; CURRENT FILING DATE: 2001-09-12  
; PRIOR FILING DATE: 2000-09-13  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: fastseq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1034  
; TYPE: DNA  
; ORGANISM: Lycopersicon esculentum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (87)...(830)  
; NAME/KEY: misc.feature  
; LOCATION: (1)...(1034)  
; OTHER INFORMATION: n = A,T,C or G

US-09-955-526-3

## Alignment Scores:

Pred. No.: 4,38e-152 Length: 1034  
 Score: 1272.00 Matches: 248  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 11 Gaps: 0

US-09-955-526-4 (1-248) x US-09-955-526-3 (1-1034)

QY 1 MetGluGlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTyrSerTyr 20  
 DB 87 ATGGAAGGTTTCACATCGTTCTTCGACTCGCAATCTGCTCTCGCAACCGTGGAGTTAT 146  
 QY 21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40  
 DB 147 GATTCCTCAAAAAGTTCGCCGAGATCTACCTCTCGTTCAAACTCATCTCAAGCAGGTG 206  
 QY 41 TyrLeuThrLeuCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60  
 DB 207 TACCTTAGCTATGCTGTGCTTTAGTGGCATGGCTGTGGGCTTACCTTCACATTTCTA 266  
 QY 61 TrpAsnIleGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTyrLeuLeu 80  
 DB 267 TGAATATCGGTGGCTCTCTCAACAATGGCTTCGATGGGAGCATGGTGGCTTCTC 326  
 QY 81 SerAlaProTyrGlnGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100  
 DB 327 TCAGTCTCCTCTATCAAGAGCAAAAAGGTGGCTCTTCGATGGCAGCTGCATTTT 386  
 QY 101 GluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleVal 120  
 DB 387 GAAGCGGCTCTATTGGCTCTCTGATGAGCTGGGCATTAACCTGATCCAGCATTTGG 446  
 QY 121 PheGlyAlaPheValGlyCysAlaValPheGlyCysPheSerAlaAlaMetLeu 140  
 DB 447 TTTGGCGCTTTGTAGTTGTGCTGGTGTGTTTGGTTCTCTCAGCTGCTGCCATGTTG 506  
 QY 141 AlaArgArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSerLeuLeu 160  
 DB 507 GCAAGCGCAGGAGTACTTGTACCTCGGGGGCTCTCTTCATCTGGCTCTCCCTTCTC 566  
 QY 161 PheTrpLeuHisPheAlaSerIlePheGlyGlySerMetAlaValPheLysPheGlu 180  
 DB 567 TTCCTGGTGCATCTTGCACTCCCATTTTGGTGGTTCCATGGCTTTTCAAGTTTGA 626  
 QY 181 LeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluIle 200  
 DB 627 TTGTATTTTGGACTCTTGGTGTGTTGTGGCTACATGCTTTTGACACCCCAAGAAATAT 686  
 QY 201 GluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThrAsp 220  
 DB 687 GAGAAGGCTCACTTGGGTGATATGGAATACGTTAAGCATGCAATGACCTTTTCACAGAT 746  
 QY 221 PheGlyAlaValPheValArgIleLeuIleMetLeuLysAsnAlaSerGluLysGlu 240  
 DB 747 TTTGGCGCTTTTGTGGGATCTTGATCATCATCATCTTAAAGATGCACTGAGAGGAA 806  
 QY 241 GluLysLysLysLysArgAsn 248  
 DB 807 GAGAAGAAGAAGAAGAGGAGAAAC 830

## RESULT 2

US-09-770-445-223

; Sequence 223, Application US/09770445  
 ; Patent No. US20020023281A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gorlach, Jorn  
 ; APPLICANT: An, Yong-Qiang  
 ; APPLICANT: Hamilton, Carol M.  
 ; APPLICANT: Price, Jennifer L.

; APPLICANT: Raines, Tracy M.  
 ; APPLICANT: Yu, Yang  
 ; APPLICANT: Rameaka, Joshua G.  
 ; APPLICANT: Page, Amy  
 ; APPLICANT: Matthew, Abraham V.  
 ; APPLICANT: Ledford, Brooke L.  
 ; APPLICANT: Woessner, Jeffrey P.  
 ; APPLICANT: Haas, William David  
 ; APPLICANT: Garcia, Carlos A.  
 ; APPLICANT: Kriker, Ted  
 ; APPLICANT: Slader, Maja  
 ; APPLICANT: Davis, Keith R.  
 ; APPLICANT: Allen, Keith  
 ; APPLICANT: Hoffman, Neil  
 ; APPLICANT: Hurdan, Patrick  
 ; TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
 ; FILE REFERENCE: 2023US (PARA-012PRV)  
 ; CURRENT APPLICATION NUMBER: US/09/770,445  
 ; CURRENT FILING DATE: 2001-01-26  
 ; PRIOR APPLICATION NUMBER: US 60/178,472  
 ; PRIOR FILING DATE: 2000-01-27  
 ; NUMBER OF SEQ ID NOS: 999  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 223  
 ; LENGTH: 1009  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; US-09-770-445-223

Alignment Scores:  
 Pred. No.: 6,22e-121 Length: 1009  
 Score: 1027.50 Matches: 193  
 Percent Similarity: 90.32% Conservatives: 31  
 Best Local Similarity: 77.82% Mismatches: 23  
 Query Match: 80.78% Indels: 1  
 DB: 9 Gaps: 1

US-09-955-526-4 (1-248) x US-09-770-445-223 (1-1009)

QY 1 MetGluGlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTyrSerTyr 20  
 DB 38 ATGGAATGCGTTCCT 94  
 QY 21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40  
 DB 95 GATTCCTTAAAAACTTCCGTCAGATTTCTCCAGCGGTTCCAGAAATCATCTCTAAACGGT 154  
 QY 41 TyrLeuThrLeuCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60  
 DB 155 TATTTGACCTTATGTTGCTCTCTGTCGCTCTGCTCTTTGGAGCTTACCTCATGTGCTC 214  
 QY 61 TrpAsnIleGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTyrLeuLeu 80  
 DB 215 TGAATATCGCGGTATCTTTCACAGCATTTGATGATTTGGAACTATGATTTGGCTCTT 274  
 QY 81 SerAlaProTyrGlnGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100  
 DB 275 TCATGTCCTCTTATGACACCAAAAAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 334  
 QY 101 GluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleVal 120  
 DB 335 GAAGTGTCTTCTGTTGGCCCTTGATCAAAAGTGGCAATGATGTTGTCGCTGCTGCTCT 394  
 QY 121 PheGlyAlaPheValGlyCysAlaValPheGlyCysPheSerAlaAlaMetLeu 140  
 DB 395 ATCAGTTCGCTTGTGGAGCTGGATAGCTTGTCTGTCTTCACAGCAGCAATGTTA 454  
 QY 141 AlaArgArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSerLeuLeu 160  
 DB 455 GCAAGACGACGAGGAGTATCTCTACCTTGGAGGACTGCTTTCATCTGCTGCTATGCTA 514  
 QY 161 PheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGlu 180

QY	84	ProTyrGlnGluGlnLysArgValAlaLeuLeuMetAlaAlaLeuPheGluGlyAla	103
Db	238	CCCTTTGAAGAGAGAGAGAGGTCACCTTTGTGTGATGGCCGACATCACTGTTTCAGGCGTCC	297
QY	104	SerIleGlyProLeuIleGluLeuGlyTleAsnPheAspProSerIleValPheGlyAla	123
Db	298	TCCTATTGGACCCTTGATTGATTGGCTATTCAATCGATCCAGCCCTATCTTTAGTGCA	357
QY	124	PheValGlyCysAlaValPheGlyCysPheSerAlaAlaMetLeuAlaArgArg	143
Db	358	TTTGTGGGAACAGCTTTGGCTTTGCATGCTTCTCAGGAGCAGCTTTGGTTGCAAGCGCT	417
QY	144	ArgGluTyrLeuTyrLeuGlyCysLeuLeuSerSerglyValSerLeuLeuPheTrpLeu	163
Db	418	AGGGAGTACCTGATACCTTGGTGGCTTGGTTTCTTGGATTTGCCATCTCTCTGGTTG	477
QY	164	HisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGluLeuTyrPhe	183
Db	478	CACCTTTGCTTCTCCATCTTTGGAGGCTCAACAGCTCTCTTTAAGTTTGAGTTGTACTTT	537
QY	184	GlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluIleIleGluLysAla	203
Db	538	GGGCTATTGGTGTTTGTAGGTACATTGTAGTAGACACCCCAAGAAATAGTTGAGAGGGCA	597
QY	204	HisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThrAspPheGlyAla	223
Db	598	CACCTTGGGGGATCTGGCATNTGTAAAGCATGCCCTTGACCTTGTTTACCGATTTGGTCGCA	657
QY	224	ValPheValArgIleLeuIleMetLeuLysAsnAlaSerGluLysGluGluLysLys	243
Db	658	GTTTGTTCGGATCTTGTATTATGTTGAAGAATTCGACTGAGAGGAATGAGAGAAA	717

DD

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184 GlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluIleIleGluLysAla 203
Db 538 GGGCTATTGGGTCTTTGTAGTTACATTGTAGTACACACCCCAAGAAATAGTTGAGAGGCCA 597
QY 204 HsLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThrAspPheGlyAla 223
Db 598 CACTTGGGGGATCTGGCATGTGTAAGCATGCCCTTGACCTTGTTTACCGATTTGGTCGCA 657
QY 224 ValPheValArgIleLeuIleIleMetLeuLysAsnAlaSerGluLysGluGluLysLys 243
Db 658 GTTTTTCGGGATCTCTGTATTATGTTGAAGAAATTCGACTGAGAGGAATGAGAAGAA 717
QY 244 LysLysArgArgAsn 248
Db 718 AAGAAGAGAAGAGAT 732

RESULT 4
US-10-219-220-232
; Sequence 232, Application US/10219220
; Publication NO. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of plant develo
; FILING DATE: 2000

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;  
;  
;

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; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 232
; LENGTH: 1218

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TYPE	ORGAN
;	;

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US-10-219-220-232
Alignment Scores:
Pred. No.:          Length:      1218
Score:              Matches:      186
Percent Similarity: 85.20%         Conservative: 27
Best Local Similarity: 74.40%      Mismatches: 32
Query Match:        75.75%         Indels: 5
DB:                  14            Gaps: 2

US-09-955-526-4 (1-248) x US-10-219-220-232 (1-1218)

Qy      1 MetGluGlyPheThrSerPhePheApsSerGluSerAlaSerArgAsnArgTrpSerTyr 20
      |||::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      123 A*GGACGGGTTCGCTTCCTCTCCAGTCG-----AGCGGCAAGGGTGGAGCCAC 173

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aSerArgAsnArgTrpSerTyr 20  
||| |||||:::  
-AGCGGCAAGGGGTGGAGCCAC 173  
lGlnThrHisLeuLysGlnVal 40



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; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (72)...(830)
US-10-167-015-31

Alignment Scores:
Pred. No.: 1.08e-102 Length: 1026
Score: 884.50 Matches: 166
Percent Similarity: 80.80% Conservative: 36
Best Local Similarity: 66.40% Mismatches: 41
Query Match: 69.54% Indels: 7
Gaps: 2
DB: 14

US-09-955-526-4 (1-248) x US-10-167-015-31 (1-1026)

QY 6 SerPheAspSerGlnSerAlaSer-----ArgAsnArgTrpSer 19
Db 78 GCGTCTCTCGGCTCTCTCGGCTCGGCGGCCCTACGGCTACGGCGCGCGGATGGAGC 137

QY 20 TyrAspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGln 39
Db 138 TAGGACTCGCTCAAGAACTTCGCGCAGATACCCCGCGCTCCAGACCCACCTCAAGCTC 197

QY 40 ValTyrLeuThrLeuLysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIle 59
Db 198 GTCTACCTACCTCTGTGCGCGCGCTGCGCTGCGCGGTGGCGCTTACCTGCACGCTG 257

QY 60 LeuTyrAsnIleGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeu 79
Db 258 GTCGTGACATCGGCGGTACGCTGACATGCTCGGTGCGGTGCGGCGATCGCTGGCTC 317

QY 80 LeuSerAlaProProTyrGlnGluGlnLysArgValAlaLeuLeuMetAlaAlaLeu 99
Db 318 TTCTCGGTGCGCGCTACGAGGAGAGAGAGATGATGGCTGCTGATGGCGGCTCGCCTC 377

QY 100 PheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIle 119
Db 378 CTGGAGGCGCTTCGGTCGGACCCCTCGTCAAGCTCGCGGTGGAATTTGACCAAGCATC 437

QY 120 ValPheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaAlaMet 139
Db 438 CTGGTGACGGGCTTCGTGGGACTGCCATCGGTTCGGCTGCTTACCGCGCGGCGCAATG 497

QY 140 LeuAlaArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSerLeu 159
Db 498 GTGGCAGCGCAGGAGTACCTCTACCTGGGTGGGCTGCTCTCGTGGGCGCTCCCATC 557

QY 160 LeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheIlysthe 179
Db 558 CTGCTCTGGCTGCACACTACCGCGGCTCCATCTTCGGCCACTCCGCAACAGCTCATGTC 617

QY 180 GluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluIle 199
Db 618 GAGGTCTACTTGGGCTGCTCATCTCTGGGCTACGTGGGTAGTACGACCGAGGATC 677

QY 200 IleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThr 219
Db 678 ATCGAGAGGGCGCACCGCGCGGACATGGACCGTCAAGCAGCGCCCTCACCCCTCTTCACA 737

QY 220 AspPheGlyAlaValPheValArgIleLeuIleMetLeuLysAsnAlaSerGluLys 239
Db 738 GACTTCGTGGCGGCTCTCTCGGCTCGGCTCTCGTCATCATGCTCAAGACGGGCGGCAAG 797

QY 240 ---GluGluLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 248
Db 798 TCGGAGGACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 827

RESULT 7
US-10-167-015-33
; Sequence 33, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 1138
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (136)...(912)
US-10-167-015-33

Alignment Scores:
Pred. No.: 6.37e-102 Length: 1138
Score: 879.00 Matches: 166
Percent Similarity: 80.00% Conservative: 42
Best Local Similarity: 63.85% Mismatches: 40
Query Match: 69.10% Indels: 12
Gaps: 3
DB: 14

US-09-955-526-4 (1-248) x US-10-167-015-33 (1-1138)

QY 1 MetGluGlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArg----- 17
Db 127 TTGGCAGGATGGAGCGGCTTCTACTCGACCGCGCTCTCTCTCTCTCTCTCTCTCTCT 186

QY 18 -----TrpSerTyrAspSerLeuLysAsnPheArgGlnIleSer 30
Db 187 TACGCGCGCGCGCGGCGGAAAGGCTGGGCTACGACTCGATGAAGAACTTCGCCAGATCAGC 246

QY 31 ProLeuValGlnThrHisLeuLysGlnValTyrLeuThrLeuLysCysAlaLeuValAla 50
Db 247 CCGCGCGGTCGACACCCCTCAAGCTGCTTTACCTCACCCCTATGCTGCGCGGCTGCGCTG 306

QY 51 SerAlaAlaGlyAlaTyrLeuHisIleLeuTyrAsnIleGlyGlyLeuLeuThrThrMet 70
Db 307 TCGGCGGTGGGCGGCTACTGCGCGCTGCTGGAACATCGCGCGGATGCTGACCATGCTC 366

QY 71 AlaCysMetGlySerMetValTrpLeuLeuSerAlaProProTyrGlnGluIleLysArg 90
Db 367 GCGTCGCTCGGCGGATCGCTGCTTCTCGGTGCGGCTCTACGAGGAGAGAGAGAGAG 426

QY 91 ValAlaLeuLeuMetAlaAlaLeuPheGluGlyAlaSerIleGlyProLeuIleGlu 110
Db 427 TACTGGCTGCTGATGCGGCTCCCTCTCTGGAAGGCGGCTGGTGGACCCCTCATCAAG 486

QY 111 LeuGlyIleAsnPheAspProSerIleValPheGlyAlaPheValGlyCysAlaValVal 130
Db 487 CTCGCGCGGAAATTTGACCAAGCATCTTGGTGACAGCGTTCTGTTGGGACTGCGCATTCG 546
```





Percent Similarity: 80.00% Conservativity: 36  
Best Local Similarity: 65.60% Mismatches: 43  
Query Match: 68.47% Indels: 7  
DB: 14 Gaps: 1

US-09-955-526-4 (1-248) x US-10-167-015-3 (1-1026)

```
QY 6 SerPheAspSerGlnSerAlaSer-----ArgAsnArgTrpSer 19
DB 78 GGGTTCTTCGCGCTCCCTCCGCGCGCTACGGCTACGGCGCGCGCGCGGATGGAGC 137
QY 20 TyrAspSerLeuValAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGln 39
DB 138 TAGGACTCGCTCAGAACITCCGCCAGATCACCGCGCTCCAGACCCACCTCAAGCTC 197
QY 40 ValTyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIle 59
DB 198 GTCTACTCACCCTGTGCGCGCTGGCTCGTGGCGGTGGCGCTTACCTGCACGNG 257
QY 60 LeuTrpAsnIleGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeu 79
DB 258 GTCTGGAACATCGGGGTACGTCGACAAATGCTCGGTGCTGCGCAGCATCGCTGCCTC 317
QY 80 LeuSerAlaProTyrGlnGlnLysArgValAlaLeuLeuMetAlaAlaLeu 99
DB 318 TTTCTGGTCCCGCTACAGGAGGAGGAGAGATGAGGCTGCTGATGGCGGTGCGCTC 377
QY 100 PheGluGlyAlaSerIleGlyProLeuLeuGluLeuLysIleAsnPheAspProSerIle 119
DB 378 CTGGAAGGCGCTCGGTGCGACCCCTCGTCAAGCTCGCGTGGAAATTTGACCCCAAGCATC 437
QY 120 ValPheGlyAlaPheValGlyCysAlaValAlaValPheGlyCysPheSerAlaAlaMet 139
DB 438 CTGGTGACCGGCTTCGCGGACTGCCATCGCGTTCGCGTGTTCACCGCGCGCGCATG 497
QY 140 LeuAlaArgArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSerLeu 159
DB 498 GTGGCAGCGCGCAGGAGTACCTTACCTGGTGGTGGCTCTCTCGTGGGGTCTCCATC 557
QY 160 LeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPhe 179
DB 558 CTGCTTGCTCGACGTAGCGGCTCCATCTTCGCGCCTCGCAACACCTTCATGTTC 617
QY 180 GluLeuTyrPheGlyLeuValPheValGlyTyrIleValPheAspThrGlnGluIle 199
DB 618 GAGGCTACTTCGGCTGCTATCTTCCTCGGCTAGCTGCTGTACACACGAGGAGATC 677
QY 200 IleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThr 219
DB 678 ATCGAGAGGCGCACCGCGCGCACATGGACACGTCACGACGCGCTCACCCTCTTCACA 737
QY 220 AspPheGlyAlaValPheValArgIleLeuIleMetLeu-LysAsnAlaSerGluLys 239
DB 738 GACTTCGTGGCGCTCGTCTCGCGCTTCCTGCTCATCTGCTCAATGCTCAAAAGACGGGCGC 797
QY 239 sGluGluLysLysLysArgArgAsn 248
DB 798 GTGCGGAGGACAGAGAGAGAGAGAGT 825
```

## RESULT 10

US-10-167-015-1  
; Sequence 1, Application US/10167015  
; Publication No. US20030056249A1  
; GENERAL INFORMATION:  
; APPLICANT: Simmons, Carl R.  
; APPLICANT: Gordon-Kamm, William J.  
; APPLICANT: Johal, Gurmukh  
; APPLICANT: Acevedo, Pedro A. Navarro  
; APPLICANT: Tao, Yumin  
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use  
; TITLE OF INVENTION: Thereof  
; FILE REFERENCE: 1388  
; CURRENT APPLICATION NUMBER: US/10/167,015

; CURRENT FILING DATE: 2002-06-11  
; PRIOR APPLICATION NUMBER: US 60/297,478  
; PRIOR FILING DATE: 2001-06-12  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 957  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (72)...(823)  
US-10-167-015-1

## Alignment Scores:

Pred. No.: 3,03e-90 Length: 957  
Score: 786.50 Matches: 158  
Percent Similarity: 78.69% Conservativity: 34  
Best Local Similarity: 64.75% Mismatches: 45  
Query Match: 61.83% Indels: 7  
DB: 14 Gaps: 3

US-09-955-526-4 (1-248) x US-10-167-015-1 (1-957)

```
QY 11 GlnSerAlaSerArgAsnArg-----TrpSerTyrAspSerLeuLysAsnPheArg 27
DB 90 CAATCGCAGCGAGGAGGAGCGCGCGCTTCGAATCGCTCAAGCGTCTGGGT 149
QY 28 GlnIleSerProLeuValGlnThrHisLeuLysGlnValTyrLeuThrLeuCysAla 47
DB 150 CACAUCTCACCGCGTGTGAGTCCACCTCAACACTGCTACCTACCTATGCTCCGG 209
QY 48 LeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrpAsnIleGlyLeuLeu 67
DB 210 GTTGGCTTCTCGACCTCGCGGTACCTCCACATCTCTCAACGTCGAGCGCGCTC 269
QY 68 ThrThrMetAlaCysMetGlySerMetValTrpLeuLeuSerAlaProTyr----- 85
DB 270 AGACCGTGGGATGCGTGGCTCCATCTCTCATCTCTGCTGCTGCTGCTGCTGCTG 329
QY 86 GlnGluGlnLysArgValAlaLeuLeuMetAlaAlaAlaLeuPheGluGlyAlaSerIle 105
DB 330 CAGGAGAGGAGACCGCTGGCGTGTCTCATGTCTGCGCGCTCTCTTCAAGCGCGTCC 389
QY 106 GlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleValPheGlyAlaPheVal 125
DB 390 GTTCCGCTCGTGGCTGCTGCTTATTTGATTCGAGGATTCCTGCTCATCTGCTGCTC 449
QY 126 GlyCysAlaValValPheGlyCysPheSerAlaAlaAlaMetLeuAlaArgArgGlu 145
DB 450 GGGACCGCAGTTCCTTTTCATGCTTCTGCGCTGCTCATCTGCGCTGCTGCTGCTG 509
QY 146 TyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSerLeuLeuPheTrpLeuHisPhe 165
DB 510 TACCTGTACTCGCGGTGCTGCTTTCATCTGCGCTCTCATCTCTCTGCTGCTGCTG 569
QY 166 AlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGluLeuTyrPheGlyLeu 185
DB 570 GCTACTTCAATCTTTGGCCACACCGCGCGCTTCATCTGCTGCTGCTGCTGCTGCT 629
QY 186 LeuValPheValGlyTyrIleValPheAspThrGlnGluIleLeuLysAlaHisLeu 205
DB 630 CTGGTTTTCCTGGGATATATGTTTGTACACCGAGGAGATCTCGAGGCGCGCACCG 689
QY 206 GlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThrAspPheGlyAlaHisPhe 225
DB 690 GGGACATGGACTACATCAAGCAGCGCTGCTCTCTTCCACGACTTTGTTGCGGTCTT 749
QY 226 ValArgIleLeuIleMetLeuLysAsnAlaSerGluLys-----GluGluLysLys 243
DB 750 GTTCGAATCTCTGTCATCATGATGAAGATGACAGAGAAATCCCAAGACGAGAGAG 809
QY 244 LysLysArgArg 247
```

Db 810 AGGAAGAAGCGG 821  
 RESULT 11  
 US-10-219-220-231  
 ; Sequence 231, Application US/10219220  
 ; Publication No. US20030082724A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Flinn, Barry  
 ; APPLICANT: Lasham, Annette  
 ; TITLE OF INVENTION: Compositions affecting programmed cell  
 ; TITLE OF INVENTION: death and their use in the modification of plant development  
 ; FILE REFERENCE: 11000.1022c1  
 ; CURRENT APPLICATION NUMBER: US/10/219,220  
 ; CURRENT FILING DATE: 2002-08-14  
 ; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932  
 ; PRIOR FILING DATE: 1999-06-04  
 ; NUMBER OF SEQ ID NOS: 290  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 231  
 ; LENGTH: 1102  
 ; TYPE: DNA  
 ; ORGANISM: Pinus radiata  
 US-10-219-220-231  
 Alignment Scores:  
 Pred. No.: 2,29e-88 Length: 1102  
 Score: 772.50 Matches: 153  
 Percent Similarity: 75.59% Conservatives: 39  
 Best Local Similarity: 60.24% Mismatches: 55  
 Query Match: 60.73% Indels: 7  
 DB: 14 Gaps: 3  
 US-09-955-526-4 (1-248) x US-10-219-220-231 (1-1102)  
 Qy 1 MetGluGlyPheThrSerPhe-----PheAspSerGlnSerAlaSerArgAsn 16  
 Db 92 ATGGCTTCATACGCTTCTTATTATGGCGGAGGATCCCTAACACGAGGTTTCGGTCATCCT 151  
 Qy 17 ArgTrpSerTyrAspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHis 36  
 Db 152 TCTGGGATACAACTGCTATGAAGACATCAAGAAAGATCAGCCCTGCGCTGCAGATCAT 211  
 Qy 37 LeuLysGlnValTyrLeuThrLeuTyrCysAlaLeuValAlaSerAlaGlyAlaTyr 56  
 Db 212 CTGAAGAAGGTTTATTGTTCGCTAGCTGCGCTCGTAACACGACGATCGTGTTTAT 271  
 Qy 57 LeuHisIleLeuTrpAsnIleGlyLeuLeuThrMetAlaCysMetGlySerMet 76  
 Db 272 TTGCATCTCTGTGTGAATATTGGAGGCTCCACGGGCTCGCTTGATGGTCTCTGTA 331  
 Qy 77 ValTrpLeuLeuSerAlaPro-----ProTyrGlnGluGlnLysArgValAlaLeuLeu 94  
 Db 332 ATCGGGCTCTTATCCGCTCCCTACTTCTCGAACAATGAGGCTAAGAGAGCTCGCTGCTC 391  
 Qy 95 MetAlaAlaLeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsn 114  
 Db 392 CTGGCAGCTGCTCGCTTCAAGGAGCTACTCTGGGACCGCTCATCAGCGGCTCAATAT 451  
 Qy 115 PheAspProSerIleValPheGlyAlaPheValGlyCysAlaValPheGlyCysPhe 134  
 Db 452 ATTGACTCCAGTATACTGTGTAGTGGTGTGTGGGACCTCTTGGCCCTCGCTTGCCTT 511  
 Qy 135 SerAlaAlaMetLeuAlaArgArgGluTyrLeuTyrLeuGlyLeuLeuSer 154  
 Db 512 TCGGCAGACAAATCACACCGAGACGAGGAATACCTATTTTGGGAGATTATGGGC 571  
 Qy 155 SerGlyValSerLeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlySerMet 174  
 Db 572 TCGGGATACAGATATTGATGGCTGCACACTAGCATCCTCGATTTTGGTGTCTTCG 631  
 Qy 175 AlaValPheLysPheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPhe 194  
 Db 631 TCGGGATACAGATATTGATGGCTGCACACTAGCATCCTCGATTTTGGTGTCTTCG 631



```
Db 532 TGCGTTTTCAGCAACCTGTATATGGGCTGTGTGTCATGTCGTGCTTTGTCCTTTT 591
QY 195 AspThrGlnGluLeuIleGluLysAlaHisLeuGlyAspMetAspTyrVallyHisAla 214
Db 592 GATACCTCACTCATTATTGAAGGCTGAAGATGGAGTAAAGATATATATCTGCGACTGC 651
QY 215 LeuThrLeuPheThrAspPheGlyAlaValPheValArgIleLeuLeuIleMetLeuLys 234
Db 652 GTTGACCTCTCTGTGGATTTCGTAACCTCTTCAGAAAGCTCATGATGATGCTGCTGTA 711
QY 235 AsnAlaSerGluLysGluGluLysLysLys 245
Db 712 AAT-----GAGAAGGATAGAGAGAGAGAG 738
```

## RESULT 15

```
US-10-167-015-7
; Sequence 7, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 740
; TYPE: DNA
; ORGANISM: zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(489)
US-10-167-015-7
```

```
Alignment Scores:
Pred. No.: 6,46e-52 Length: 740
Score: 484.50 Matches: 93
Percent Similarity: 82.61% Conservative: 21
Best Local Similarity: 67.39% Mismatches: 23
Query Match: 38.09% Indels: 1
DB: 14 Gaps: 1
```

US-09-955-526-4 (1-248) x US-10-167-015-7 (1-740)

```
QY 112 GlyIleAsnPheAspProSerIleValPheGlyAlaPheValGlyCysAlaValValPhe 131
Db 73 GGCTGTTTTTTTCCCTCAGCATCTGTGTGACGGCGTTCGTGGGACTGCCATCGCGTTC 132
QY 132 GlyCysPheSerAlaAlaAlaMetLeuAlaArgArgGluTyrLeuTyrLeuGlyCly 151
Db 133 GCGTGCCTTCACCGCGCGGCATGGTGCCAGCGGAGGAGTACCTCTACCTGGGTGG 192
QY 152 LeuLeuSerSerGlyValSerLeuLeuPheThrLeuHisPheAlaSerSerIlePheGly 171
Db 193 CTGCTCTGCTGGGGCTCTCCATCCTCTGTGCTGTGAGTAGCGGCTCCATCTCTGGC 252
QY 172 GlySerMetAlaValPheLysPheGluLeuTyrPheGlyLeuLeuValPheValGlyTyr 191
Db 253 CACTCGGCAACACAGCTTCTGAGGTCTACTTCGGGCTGCTCATCTCTCTGGGTAC 312
QY 192 IleValPheAspThrGlnGluIleGluLysAlaHisLeuGlyAspMetAspTyrVal 211
Db 313 GTGTGTACGACGACGAGAGATCATCGAGAGGCGCACCGCGGCGACATGGACACGTC 372
```

```
QY 212 LysHisAlaLeuThrLeuPheThrAspPheGlyAlaValPheValArgIleLeuIle 231
Db 373 AAGCAGCCCTCACCCTCTTTCACAGACTTCGTGGCCGCTCCTCGCGCTCGTCAIC 432
QY 232 MetLeuLysAsnAlaSerGluLys---GluGluLysLysLysLysArgArgAsn 248
Db 433 ATGCTCAGAACCGGGGCCGACAAAGTCGGAGGACAAAGAGAGAGAGAGAGTGC 486
```

Search completed: September 22, 2003, 17:53:08  
Job time : 251 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 22, 2003, 15:28:24 ; Search time 2060 Seconds  
(without alignments)  
2925.976 Million cell updates/sec

Title: US-09-955-526-4  
Perfect score: 1272  
Sequence: 1 MEGFTSFDSASRNWSY.....LIIMLNASEKEKKRRN 248

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Zgapop 6.0 , Zgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n\_model -DEV=xlp  
-O=/cgn2\_1/USPTO.spool/US0955526/runat\_22092003.151755.12377/app\_query.fasta.1.391  
-DB=EST\_QMWT-fastcap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US0955526 -CGN 1.1 4237 @runat\_22092003.151755.12377 -NCPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEX=6 -DELEXT=7

Database : EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmd:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est4:\*  
13: gb\_est5:\*  
14: gb\_est6:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_nam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1088.5	85.6	750	10	BG124317
2	1042	81.9	655	12	BM066817
3	1032	81.1	757	14	CA811916
4	1020	80.2	596	9	AI779122
5	1016	79.9	732	13	BU023368
6	1012	79.6	706	14	CB978248
7	990	77.8	739	13	BU895008
8	961	75.6	671	12	BI933489
9	960	75.5	643	9	AW096641
10	947	74.4	646	9	AW219279
11	940	73.9	831	12	BG839316
12	933	73.3	723	13	BQ856331
13	932	73.3	647	10	BG127849
14	931	73.2	691	13	BU896719
15	931	73.2	694	13	BU867362
16	927	72.9	713	13	BQ991270
17	914	71.9	703	13	BQ863266
18	888	69.8	643	14	CA812546
19	888	69.8	726	10	BG648712
20	879.5	69.1	738	14	CB293933
21	878.5	69.1	647	10	BE577220
22	871	68.5	694	10	BG646982
23	871	68.5	1096	11	AY105656
24	870	68.4	671	14	CA825814
25	866	68.1	611	13	BU836328
26	865	68.0	592	10	BG134507
27	862	67.8	602	14	CA823531
28	858	67.5	578	13	BQ115430
29	855	67.2	626	14	CA847592
30	851	66.9	696	14	CA909307
31	846	66.5	611	12	BJ554597
32	845	66.4	590	12	BM082213
33	844	66.4	680	14	CA909308
34	843	66.3	646	14	CB347734
35	842	66.2	611	12	BJ560791
36	840	66.0	593	12	BM062746
37	840	66.0	748	13	BU100498
38	838	65.9	620	9	AI730983
39	837	65.8	621	9	AI726851
40	836.5	65.8	700	14	CD038782
41	835	65.6	619	9	AI727198
42	835	65.6	643	14	CB894392
43	834	65.6	740	13	BQ255427
44	832	65.4	681	10	BF635314
45	828	65.1	776	10	BG648573

## ALIGNMENTS

RESULT 1  
BG124317  
LOCUS  
DEFINITION  
EST469963 tomato shoot/meristem Lycopersicon esculentum cDNA clone  
ctof4l8 5' sequence, mRNA sequence.  
ACCESSION  
BG124317  
VERSION  
BG124317.1  
KEYWORDS  
EST.  
GI:12624505  
ORGANISM  
Lycopersicon esculentum (tomato)  
Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 750)  
 AUTHORS van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Utterback, T., Hansen, C., Ronning, C. and Tanksley, S.  
 TITLE Generation of ESTs from tomato shoot/meristem tissue  
 JOURNAL Unpublished  
 COMMENT Contact: CUGI  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>.

FEATURES  
 source  
 1..750  
 /organism="Lycopersicon esculentum"  
 /mol\_type="mRNA"  
 /cultivar="TA496"  
 /db\_xref="taxon:4081"  
 /clone="c10F418"  
 /tissue\_type="shoot/meristem"  
 /dev\_stage="developing shoots from 4-6wks old plants"  
 /lab\_host="SOLR"  
 /clone\_lib="tomato shoot/meristem"  
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496). Tissue was immediately frozen in liquid nitrogen."

BASE COUNT 158 a 174 c 176 g 242 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 8,68e-94 Length: 750  
 Score: 1088.50 Matches: 214  
 Percent Similarity: 98.17% Conservative: 0  
 Best Local Similarity: 98.17% Mismatches: 3  
 Query Match: 85.57% Indels: 1  
 DB: 10 Gaps: 1

US-09-955-526-4 (1-248) x BG124317 (1-750)

QY 1 MetGluGlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyr 20  
 DB 95 ATGGAAGGTTTCACATCGCTTCTCGACATCGCAATCGCTCTCGCAACGGCTGGAGTAT 154  
 QY 21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40  
 DB 155 GATTCCTCAAAAATCTCCGGCAGATCTCACCTCTCGTTCAAACTCACTCAAGCAGTG 214  
 QY 41 TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60  
 DB 215 TACCTTAGCTATGCTGTGCTTTAGTGGCATCGGCTGCTGGGCTTACCTTCACATTCTA 274  
 QY 61 TrpAsnIleGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80  
 DB 275 TGGAAATACGGTGGCTCTCTCACAAATGGCTTCATGGGAAGCATGGTGTGGCTTCTC 334  
 QY 81 SerAlaProProTyrGlnGlu---GlnLysArgValAlaLeuLeuMetAlaAlaLeu 99  
 DB 335 TCAGCTCTCTTATCAGACGACGAAAAGGGTGGCTCTCTGATGGCAGTGCATTT 394  
 QY 100 PheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIle 119  
 DB 395 TTTGAAGCGGCTCTATTGGTCTCTGATTTAGTGGGCTTGTGCTTCTGCTGCTGCCATG 454  
 QY 120 ValPheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaMet 139  
 DB 455 GGTGTTGGCGCTTTGTAGTTGCTGTGTTTGTGTTGCTTCTGCTGCTGCCATG 514  
 QY 140 LeuAlaArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSerLeu 159  
 DB 515 TTGGCAAGCGCAGGAGTACTTGTACCTCGGGGCCCTCTTTTCATCTCGGGCTCTCCCT 574  
 QY 160 LeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPhe 179  
 DB 575 CTCCTCTGGTTCACCTTTGCATCCCATTTTGTGTTTGTGTTTGTGTTTGTGTTTCAAGTT 634

QY 180 GluLeuTyrPheGlyLeuValPheValGlyTyrIleValPheAspThrGlnGluIle 199  
 DB 635 GAGTTGATTITGGACTCTTGGGTGTTGGGCTACATCGTCTTTGACACCAAGAAAT 694  
 QY 200 IleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeu 217  
 DB 695 ATTGAGAAAGCTCACTTGGGTGATGATGATTACGTTAAGCATGCAATGACCTT 748

RESULT 2  
 BM066817 655 bp mRNA linear EST 11-SEP-2002  
 LOCUS KS07018F03 KS07 Capsicum annum cDNA, mRNA sequence.  
 DEFINITION BM066817  
 ACCESSION BM066817.1 GI:22786937  
 VERSION  
 KEYWORDS  
 EST.  
 SOURCE Capsicum annum  
 ORGANISM Capsicum annum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Capsicum.  
 REFERENCE 1 (bases 1 to 655)  
 AUTHORS Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S., Hur, C.-G. and Choi, D.  
 TITLE Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen  
 JOURNAL Unpublished  
 COMMENT Contact: Doil Choi  
 Genome Research Center and National Center for Genome Information  
 Korea Research Institute of Bioscience and Biotechnology  
 P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea  
 Tel: 82-42-860-4340  
 Fax: 82-42-860-4309  
 Email: doilemail.kribb.re.kr  
 High quality sequence stop: 655.

FEATURES  
 source  
 1..655  
 /organism="Capsicum annum"  
 /mol\_type="mRNA"  
 /cultivar="Hang Keun"  
 /db\_xref="taxon:4072"  
 /tissue\_type="flower bud"  
 /dev\_stage="10 weeks after germination"  
 /clone\_lib="KS07"  
 /note="Vector: Hydri-ZAP 2.1"

BASE COUNT 124 a 160 c 161 g 210 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 2.06e-89 Length: 655  
 Score: 1042.00 Matches: 198  
 Percent Similarity: 96.74% Conservative: 10  
 Best Local Similarity: 92.09% Mismatches: 7  
 Query Match: 81.92% Indels: 0  
 DB: 12 Gaps: 0

US-09-955-526-4 (1-248) x BM066817 (1-655)

QY 2 GluGlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrpSerTyrAsp 21  
 DB 9 GAGGTTTCAGTCTGCTTTCGATCGCAATCGGCTTCTCGCAGCTCGTGAATATGAT 68  
 QY 22 SerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnValTyr 41  
 DB 69 GCTCTCAAAAATCTCCATCATCATCTCTCGTGTTCAAACTCATCTCAACAGCTCAT 128  
 QY 42 LeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrp 61  
 DB 129 CTCACATATCTGTGCTTTAGTCGATCAGCTGCTGGGCTTACCTTCACATTCTTGG 188  
 QY 62 AsnIleGlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeuSer 81  
 DB 188





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RESULT 4
AI779122
LOCUS
DEFINITION
  EST260001 tomato susceptible, Cornell Lycopersicon esculentum cDNA
  clone CLS7M13, mRNA sequence.
ACCESSION
AI779122
VERSION
AI779122.1
KEYWORDS
  EST.
SOURCE
  Lycopersicon esculentum (tomato)
ORGANISM
  Lycopersicon esculentum
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
  1 (bases 1 to 596)
  D' Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E.,
  Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman
  C.L., Nierman, W., Fraser, C.M., Venter, J.C., Tanksley, S.D.,
  Giovannoni, J.J., and Martin, G.B.
  Generation of ESTs from Pseudomonas susceptible tomato
  Unpublished
  Contact: CUGI
  Clemson University Genomics Institute
  100 Jordan Hall, Clemson, SC 29634, USA
  Email: http://www.genome.clemson.edu/orders/index.html
  5 prime sequence.
FEATURES
  source
    Location/Qualifiers
      1..596
        /organism="Lycopersicon esculentum"
        /mol_type="mRNA"
        /cultivar="R11-13 (Rio Grande x Money Maker)"
        /db_xref="taxon:4081"
        /clone="cUES7M13"
        /tissue_type="leaf"
        /dev_stage="4-week old"
        /lab_host="SOLR"
        /clone_lib="tomato susceptible, Cornell"
        /note="vector: pBluescript SK(-); Site1: EcoRI; Site2:
        XhoI; cUES - Tomato Pseudomonas Susceptible EST Library.
        Directionally cloned cDNAs inserted into pBluescript SK(-)
        at 5' end with EcoRI and 3' end with XhoI site"
BASE COUNT
  102 a 140 c 150 g 204 t
ORIGIN
Alignment Scores:
  2.36e-87 Length: 596
  Pred. No.: 1020.00 Matches: 198
  Score: 100.00% Conservative: 0
  Percent Similarity: 100.00% Mismatches: 0
  Best Local Similarity: 100.00% Indels: 0
  Query Match: 80.19% Gaps: 0
  DB: 9
US-09-955-526-4 (1-248) x AI779122 (1-596)
QY 26 PheArgGlnIleSerProLeuValGlnThrHisLeuTyrLeuThrLeuCys 45
Db 2 TTCGCCAGATCTCACCTCTCGTCAAACTCATCTCAAGCAGGTGACCTTACGCTATGC 61
QY 46 CysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrpAsnIleGlyGly 65
Db 62 TGTGCTTTAGTGGCATCGCTGCTGGGCTTACCTTCACATCTCATATGCAATATCGTGGC 121
QY 66 LeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeuSerAlaProProTyr 85
Db 122 CTCCTTCACAAAGATGGCTGTGATGGGAAGCATGGTGGTGGCTCTCTCTCAGCTCTCTAT 181
QY 86 GlnGlnGlnYsArgValAlaLeuLeuMetAlaAlaLeuPheGlnGlyAlaSerIle 105
Db 182 CAAGAGCAAAAGAGGTGGCTCTCTCTGATGGCAGCTGCATTTTGAAGGCGCTCTATT 241
QY 106 GlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleValPheGlyAlaPheVal 125

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Db 242 GGTCTCTGATTGAGCTGGGCATTAACTTCGATCAAGCATTTGTTTGGCGCTTTTSTA 301
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Db 302 GTTGTGCTGTGGTTTGGTTGCTTCTCAGCTCTGCCATGTTGGCAAGCGCAGGAG 361
QY 146 TyrLeuTyrLeuGlyLeuLeuSerSerGlyValSerLeuLeuPheTrpLeuHisPhe 165
Db 362 TACTTGTACCTCGGGGGCTTCTTTCATCTCGGCTCTCCCTTCTCTCTCTGTTGCACTTT 421
QY 166 AlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGluLeuTyrPheGlyLeu 185
Db 422 GCATCCCTCCATTTTGGTGGTTCATGGCTGTTTCAAGTTTGAGTTGATTTTGGACTC 481
QY 186 LeuValPheValGlyTyrIleValPheAspThrGlnGluIleIleGluLysAlaHisLeu 205
Db 482 TTGCTGTTTGGGCTACATCGTCTTTGACACCCCAAGAAATATTGAGAGGCTCCTTG 541
QY 206 GlyAspMetAspTyrValLysHisAlaLeuThrLeuPheThrAspPheGlyAla 223
Db 542 GGTGATATGGATTACGTTAAGCATGTCATGACCTTTTTCACAGATTTTGGCGCT 595
RESULT 5
BU023368
LOCUS
DEFINITION
  QHFI0M17.yg.ab1 QH_EFGHJ sunflower RHA280 Helianthus annuus cDNA
  clone QHFI0M17, mRNA sequence.
ACCESSION
BU023368
KEYWORDS
  EST.
SOURCE
  Helianthus annuus (common sunflower)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  asterids; campanulids; Asterales; Asteraceae; Asteroideae;
  Heliantheae; Helianthus.
  1 (bases 1 to 732)
  Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
  Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison
  P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
  Church, S., Jackson, L. and Bradford, K.
  Lettuce and Sunflower ESTs from the Compositae Genome Project
  http://compgenomics.ucdavis.edu/
  Unpublished
  Contact: Alexander Kozik [R.W.Michelmore]
  Department of Vegetable Crops, R.W.Michelmore Lab
  University of California at Davis (UCD)
  Asmundson Hall, UCD, Davis, CA 95616, USA
  Tel: 1-(530)-742-1742
  Fax: 1-(530)-752-9659
  Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
  singleton, see http://cgpdb.ucdavis.edu/ for details.
  Plate: QHFI0 row: M column: 17.
FEATURES
  Location/Qualifiers
    1..732
      /organism="Helianthus annuus"
      /mol_type="mRNA"
      /cultivar="RHA280"
      /db_xref="taxon:4232"
      /clone="QHFI0M17"
      /lab_host="E.coli"
      /clone_lib="QH_EFGHJ sunflower RHA280"
      /note="vector: pBRCNAsfIAB; The library was constructed
      from 11 different sources of RNA from a single genotype.
      Separate cDNAs were generated using primers that
      incorporated unique 5' and 3' tags to distinguish each
      source of RNA. cDNAs were then pooled, size-fractionated,
      directionally cloned into a custom medium-copy vector and
      transformations made with four size classes to minimize
      size bias. Details of each source of RNA and library
      construction can be obtained at http://cgpdb.ucdavis.edu/
      TAG_LIB=QH_EFGHJ sunflower RHA280
      TAG_TISSUE=hulls

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

b7d

1 TCATATGAAGAGAAAAAGAGGGTTTCACTATTGATCG

1 TCATATGAAGAGAAAAAGAGGGTTTCACATATGATGGCTGTGGCCCTTTTCAAGAGGCC 300

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QY 104 SerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleValPheGlyAla 123
DB TCTATCGGCTCTTTGATGATGCTTGGCTATTGAAATGACCAAGCATCTTGTAGTGGCT 360
QY 124 PheValGlyCysAlaValValPheGlyCysPheSerAlaAlaMetLeuAlaArgArg 143
DB TTTGTGGGAACGTCAGTGGCTTGGCTTGGCTTGGCTGCTGCAATGTTGGCAAGGGCC 420
QY 144 ArgGluTyrLeuTyrLeuGlyCysLeuLeuSerSerGlyValSerLeuLeuPheTyrLeu 163
DB AGAGAGTACCTGTATCTGGGAGGGGTTCTTCCCTGCGCCCTCCATCCCTTTCTGGFTG 480
QY 164 HisPheAlaSerSerIlePheGlyCysLeuLeuValPheLeuLysPheGluLeuTyrPhe 183
DB CACITTTGGCTCTCGTGTGTTGGGGGATCCACTGCCATCTTATGTTGAGTTGATTTT 540
QY 184 GlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluIleGluLysAla 203
DB GGACTGTTGGTGTGTTGGCTACATGTAGTACACCCAGGACATAATAGAGAAAGCC 600
QY 204 HisLeuGlyAspMetAspTyrValIleHisAlaLeuThrLeuPheThrAspPheGlyAla 223
DB CATCTCGGGGATCGGGACTATGTGAACATCTCTCCCTTTTTCACATGATTTTGTCTGCA 660
QY 224 ValPheValArgIleLeuIleMetLeuLysAsnAlaSerGlu 238
DB GTTTTGTTCGAATCTCATATCATGTTGAAGAACTCGGCTGAA 705

RESULT 7
BU995008 739 bp mRNA linear EST 17-OCT-2002
LOCUS X018A11 Populus wood cDNA library Populus tremula x Populus
DEFINITION tremuloides cDNA 5 prime, mRNA sequence.
ACCESSION BU995008
VERSION BU995008.1 GI:24106073
KEYWORDS EST.
SOURCE Populus tremula x Populus tremuloides
ORGANISM Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Malpighiales; Salicaceae; Populus.
REFERENCE 1 (bases 1 to 739)
AUTHORS Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
TITLE The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
JOURNAL Unpublished
COMMENT Contact: BHALERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.

FEATURES
source
1..739
/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/tissue_type="wood"
/clone_lib="Populus wood cDNA library"

BASE COUNT 150 a 179 c 166 g 244 t
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Alignment Scores:
Pred. No.: 2,09e-84 Length: 739
Score: 990.00 Matches: 190
Percent Similarity: 89.18% Conservative: 16
Best Local Similarity: 82.25% Mismatches: 25
Query Match: 77.83% Indels: 0
DB: 13 Gaps: 0

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US-09-955-526-4 (1-248) x BU995008 (1-739)

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QY 1 MetGluGlyPheThrSerPheAspSerGlnSerAlaSerArgAsnArgTyrSerTyr 20
DB ATGACGGCTTCGGTTCCTCTTTGACTCTCAATCGGCTTCAACGAACGGTTGGAGCTAC 105
QY 21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40
DB GATTCTCTCAAGAACTTACGCCAGATCTCTCTCTGTCTCCAGAACCACTCTCAAGCAGTT 165
QY 41 TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60
DB CATCTGACCTTATGTTGCACTGGTTCATCTCCGCTGGGGCATACCTCCATATTCTG 225
QY 61 TrpAsnIleGlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTyrPheLeu 80
DB TGGATATGTTGGTCTCTTAAACGACATCCCAAGCTTGGATGATGCTTGGCTACTT 285
QY 81 SerAlaProProTyrGlnGlnGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100
DB TCCATATCTCCTTATGAAGAGCAAAAGAGGTTGGTCTCTTGTATGGCAACGCACCTTC 345
QY 101 GluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleVal 120
DB CAAGGGGCTTCTATAGGTCCTCTGATGATCTGGCAATCAGATTGATCCCAAGTGTCTG 405
QY 121 PheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaMetLeu 140
DB ATTACAGCTTTTGTGGGAACCTCGGCTAGCTTTGGATGTTCTCAGTAGCAGTATGTTG 465
QY 141 AlaArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSerLeuLeu 160
DB GCTAGCGCTAGAGATAATCTTACTTGGTGGCTTGTCTTCATCGGCTTTCATCTCT 525
QY 161 PheTyrLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGlu 180
DB CTATGGCTGCATTTGGCATCTCCATCTTGGGGATCTGGAGCTCTTTAAATTGAG 585
QY 181 LeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluLeu 200
DB CTGTACTTTGGGCTCTCTGGTGTGTTGGGCTATGTTGGTAGTTGACACCCAGGATATCAT 645
QY 201 GluLysAlaHisLeuGlyAspMetAspTyrValIleHisAlaLeuThrLeuPheThrAsp 220
DB GAGAAAGCTCACCCTGGTGTGATCTGGACATGTAAGACATTCCTCGAGCTTTTCACAGC 705
QY 221 PheGlyAlaValPheValArgIleLeuIleLeu 231
DB TTCGTTGCTGTTTGTCCGAATTCCTATAATC 738

BI933489 671 bp mRNA linear EST 18-OCT-2001
EST553378 tomato flower, anthesis Lycopersicon esculentum cDNA
clone cTOD16N14 5' end, mRNA sequence.
BI933489
VERSION BI933489.1 GI:16247961
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 671)
van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J.,
Utterback, T., Van Aken, S., Ronning, C.M., Nierman, W., Fraser, C.M.,
Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from tomato flower tissue, anthesis (2001)
Contact: CUGI
Unpublished
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html

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This clone is available through the Clemson University Genomics Institute  
 Seq primer: r3.

# FEATURES

Source  
 Location/Qualifiers  
 1..671  
 /organism="Lycopersicon esculentum"  
 /mol\_type="mRNA"  
 /cultivar="TA496"  
 /db\_xref="taxon:4081"  
 /clone="cT0016N14"  
 /tissue\_type="flower"  
 /dev\_stage="anthesis"  
 /clone\_lib="tomato flower, anthesis"  
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Cornell University; sequencing: The Institute for Genomic Research; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."  
 BASE COUNT 134 a 161 c 157 g 219 t  
 ORIGIN

## Alignment Scores:

Pred. No.: 1..11e-81 Length: 671  
 Score: 961.00 Matches: 196  
 Percent Similarity: 98.49% Conservative: 0  
 Best Local Similarity: 98.49% Mismatches: 3  
 Query Match: 75.55% Indels: 2  
 DB: 12 Gaps: 0

US-09-955-526-4 (1-248) x B1933489 (1-671)

QY 1 MetGluGlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrrpSerTyr 20  
 Db ATGGAAGGTTTCACATCGTTCTTCGACTCGCAATCGCTCTCGCAACCGCTGGAGTTAT 135  
 QY 21 AspSerLeuLysAspPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40  
 Db GATTCTCTCAAAACCTTCGCGCAGATCTCACCTCTCGTTTCAAACTCATCTCAAGCAGGTF 195  
 QY 41 TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60  
 Db TACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTCTCGGGGCTTACCTTCACATTCTA 255  
 QY 61 TrpAsnIleGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80  
 Db TGGAAATATCGTGGCTCTCTCAACAATGGCTTGCATGGGAAGCATGGTGGCTTCTC 315  
 QY 81 SerAlaProTyrGlnGluGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100  
 Db TCAGCTCTCCCTTATCAAGAGCAAAAGGGTGGCTCTTCTGATGGCAGCTGCACCTTTT 375  
 QY 101 GluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleVal 120  
 Db GAAGCGCCTCTATTGGTCTCTGATTGAGCTGGGCATTAACTTCATCAAGCATTTGG 435  
 QY 121 PheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaAlaMetLeu 140  
 Db TTTGGCGCTTTTGTAGTTGTCTGTGGTTTGTGGTTTGTCTCAGCTCTGCCATGTTG 495  
 QY 141 AlaArgArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSerLeuLeu 160  
 Db GCAAGCGCAGGAGTACTTGTACCTCGGGGGCCCTCTTTTCACTCGGGCTCTCCCTTCTC 555  
 QY 161 PheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGlu 180  
 Db TTCTGGTTGCACTTTGCACTCTCCATTTTGTGTGTTTCAAGTTTCAAGTTT-GAG 613  
 QY 181 LeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluLe 199  
 Db TTGATTTTGGACTCTTGGTGGTTTGGGCTACATCGTCTTTTGACACCCCAAGAAATT 670

RESULT 9

AW096641

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

Source

Location/Qualifiers

1..643

/organism="Lycopersicon esculentum"

/mol\_type="mRNA"

/cultivar="Rio Grande PtoR"

/db\_xref="taxon:4081"

/clone="cLET39W7"

/tissue\_type="leaf"

/dev\_stage="4-6 week old plants"

/lab\_host="XLI-Blue MRP"

/clone\_lib="tomato mixed elicitor, BTT"

/note="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2: XhoI; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenthion, EHX, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

BASE COUNT 129 a 155 c 150 g 209 t

ORIGIN

Alignment Scores:

Pred. No.: 1.32e-81 Length: 643

Score: 960.00 Matches: 186

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 75.47% Indels: 0

DB: 9 Gaps: 0

US-09-955-526-4 (1-248) x AW096641 (1-643)

QY 1 MetGluGlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrrpSerTyr 20

Db ATGGAAGGTTTCACATCGTTCTTCGACTCGCAATCGCTCTCGCAACCGCTGGAGTTAT 144

QY 21 AspSerLeuLysAspPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40

Db GATTCTCTCAAAACCTTCGCGCAGATCTCACCTCTCGTTTCAAACTCATCTCAAGCAGGTF 204

QY 41 TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60

Db TACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTCTCGGGGCTTACCTTCACATTCTA 264

QY 61 TrpAsnIleGlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80

Db TGGAAATATCGTGGCTCTCTCAACAATGGCTTGCATGGGAAGCATGGTGGCTTCTC 324

QY 81 SerAlaProTyrGlnGluGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100

Db TTTGATTTTGGACTCTTGGTGGTTTGGGCTACATCGTCTTTTGACACCCCAAGAAATT 670

AW096641 643 bp mRNA linear EST 18-MAY-2001  
 EST289821 tomato mixed elicitor, BTT Lycopersicon esculentum cDNA  
 clone cLET39M7, mRNA sequence.

AW096641  
 AW096641.1 GI:6062236  
 EST.

Lycopersicon esculentum (tomato)  
 Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 643)  
 D'Ascenzo,M., He,X., Lyman,J., Holt,I.E., Liang,F., Upton,J.,  
 Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W.,  
 Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni  
 ,J.

Generation of ESTs from tomato leaf tissue  
 Unpublished  
 Contact: CUGI  
 Clemson University Genomics Institute

Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>

5 prime sequence.

FEATURES

Location/Qualifiers

1..643

/organism="Lycopersicon esculentum"

/mol\_type="mRNA"

/cultivar="Rio Grande PtoR"

/db\_xref="taxon:4081"

/clone="cLET39W7"

/tissue\_type="leaf"

/dev\_stage="4-6 week old plants"

/lab\_host="XLI-Blue MRP"

/clone\_lib="tomato mixed elicitor, BTT"

/note="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2: XhoI; cLET - Inoculated with a variety of disease response

elicitors. Plants exposed to 2,6 dichloroisonicotinic

acid, BTH, jasmonic acid, ethylene, fenthion, EHX,

okadaic acid, or systemin prior to tissue harvest. EcoRI

site was destroyed during cloning."

BASE COUNT 129 a 155 c 150 g 209 t

ORIGIN

Alignment Scores:

Pred. No.: 1.32e-81 Length: 643

Score: 960.00 Matches: 186

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 75.47% Indels: 0

DB: 9 Gaps: 0

US-09-955-526-4 (1-248) x AW096641 (1-643)

QY 1 MetGluGlyPheThrSerPhePheAspSerGlnSerAlaSerArgAsnArgTrrpSerTyr 20

Db ATGGAAGGTTTCACATCGTTCTTCGACTCGCAATCGCTCTCGCAACCGCTGGAGTTAT 144

QY 21 AspSerLeuLysAspPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40

Db GATTCTCTCAAAACCTTCGCGCAGATCTCACCTCTCGTTTCAAACTCATCTCAAGCAGGTF 204

QY 41 TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60

Db TACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTCTCGGGGCTTACCTTCACATTCTA 264

QY 61 TrpAsnIleGlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80

Db TGGAAATATCGTGGCTCTCTCAACAATGGCTTGCATGGGAAGCATGGTGGCTTCTC 324

QY 81 SerAlaProTyrGlnGluGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100

Db TTTGATTTTGGACTCTTGGTGGTTTGGGCTACATCGTCTTTTGACACCCCAAGAAATT 670

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Db      325 TCAGTCTCTCTTATCAAGAGCAAAAAAGGGTGGCTCTTCTGATGGCAGCTGCACCTTTT 384
Qy      101 GluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleVal 120
Db      385 GAAGGCGCTCTATGGGCCCTGATGAGCTGGGCACTAACTTCGATCCAAGCATTTGG 444
Qy      121 PheGlyAlaPheValGlyCysAlaValPheGlyCysPheSerAlaAlaAlaMetLeu 140
Db      445 TTTGGCGCTTTGTAGGTGTGCTGTGTTTGGTTCCTCAGCTGCTGCCATGTTG 504
Qy      141 AlaArgArgGluTyTyLeuTyTyLeuGlyGlyLeuLeuSerSerGlyValSerLeuLeu 160
Db      505 GCAAGGCGCAGGAGTACTTACCTCGGGGCGCTCTTTCATCTGGCGTCTCCCTTCTC 564
Qy      161 PheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGlu 180
Db      565 TTCGTGGTGCACCTTTCATCTCCATTTTGGTGTTCATCGGCTGTTTCAAGTTTGG 624
Qy      181 LeuTyPheGlyLeuLeu 186
Db      625 TTGTATTTGGACTCTTG 642

RESULT 10
AW219279
LOCUS   646 bp      mRNA      linear      EST 18-MAY-2001
DEFINITION
Lycopersicon esculentum cDNA clone cLEX3N8, mRNA sequence.
ACCESSION
AW219279.1 GI:6530153
VERSION
1
KEYWORDS
Lycopersicon esculentum (tomato)
SOURCE
Lycopersicon esculentum
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 646)
van der Hoeven,R.S., Garvin,D., Matern,A.L., Holt,I.E., Liang,F.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Renning,C.M.,
Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
Generation of ESTs from tomato root tissue
Unpublished
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.

FEATURES
source
1..646
Location/Qualifiers
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEX3N8"
/tissue_type="root"
/dev_stage="plants during and after fruit-set"
/clone_lib="tomato root during/after fruit set, Cornell
University"
/notes="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Tanksley; Tissue supplied by Dave Garvin
(USDA-ARS, Ithaca, NY 14850)."
```

BASE COUNT  
ORIGIN

Alignment Scores:

Pred. No.: 2 31e-80 Length: 646  
Score: 947.00 Matches: 186  
Percent Similarity: 99.47% Conservative: 0  
Best Local Similarity: 99.47% Mismatches: 0  
Query Match: 74.45% Indels: 1  
DB: 9 Gaps: 0

US-09-955-526-4 (1-248) x AW219279 (1-646)

```

Qy      1 MetGluGlyPheThrSerPheAspSerGlnSerAlaSerArgAsnArgTyrSerTyr 20
Db      87 ATGAAGGTTTCACATCGTTCTTCGACGCAATCGCTCTCGCAACCGCTGGAGTTAT 146
Qy      21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40
Db      147 GATTCTCTCAAAAACTTCGCGCAGATCTCAGCTCTCGTTCAAACTCACTCAAGCAGGTG 206
Qy      41 TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyTyLeuHisLeuLeu 60
Db      207 TACCTTAGCTATGCTGTGCTTTAGTGGCATCGGCTGCTGGGCTTACCTTCACATTCTA 266
Qy      61 TrpAsnIleGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
Db      267 TGGAAATATCGTGGCTCTCTCACAAATGCTTGCATGGGAAGCATGGTGGGTTCTC 326
Qy      81 SerAlaProProTyTyGlnGlnLysArgValAlaLeuLeuMetAlaAlaLeuPhe 100
Db      327 TCAGCTCTCTCTTATCAAGAGCAAAAAAGGGTGGCTCTTCTGATGGCAGCTGCACCTTTT 386
Qy      101 GluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleVal 120
Db      387 GAAGGCGCTCTATGGTCTCTCTGATTGAGCTGGGCACTAACTTCGATCCAAGCATTTG 446
Qy      121 PheGlyAlaPheValGlyCysAlaValPheGlyCysPheSerAlaAlaAlaMetLeu 140
Db      447 TTTGGCGCTTTTGTAGTTGTCTGTTTGGTGTCTTCTCAGCTGCTGCCATGTTG 506
Qy      141 AlaArgArgGluTyTyLeuTyTyLeuGlyGlyLeuLeuSerSerGlyValSerLeuLeu 160
Db      507 GCAAGGCGCAGGAGTACTTGTACCTCGGGGCTCTTTCATCTGCGGCTCTCCCTTCTC 566
Qy      161 PheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPhe-LysPheG 180
Db      567 TTCGTGGTGCACCTTTCATCTCCATTTTGGTGGTTCATGCGCTGTTTCAAACTTGA 626
Qy      180 uLeuTyPheGlyLeuLeu 186
Db      627 GTGTATTTGGACTCTTG 645

RESULT 11
BG839316 831 bp      mRNA      linear      EST 25-MAY-2001
LOCUS   Gm01_16b10_A Gm01_AAFCECORC_Glycine_max_cold_stressed_leaves
DEFINITION
Glycine max cDNA clone Gm01_16b10, mRNA sequence.
ACCESSION
BG839316
VERSION
BG839316.1 GI:14205638
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 831)
Singh,J.A., Robert,L.S., Lu,B., Zhu,L., De Moors,A., Couroux,P.,
Harris,L.J., Hattori,J.I., Ouellet,T., Spratt,D. and Tinker,N.A.
Expressed Sequence Tags from Cold-Stressed Glycine max (soybean)
Leaves
Unpublished
Contact: Singh,J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neathy Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
0C6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca.
Location/Qualifiers
1..831
/organism="Glycine max"
/mol_type="mRNA"
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/cultivar="Maple Arrow"  
 /db\_xref="taxon:3847"  
 /clone="Gm01\_16b10"  
 /tissue\_type="Leaves"  
 /dev\_stage="15-day seedlings"  
 /clone\_lib="Gm01\_AAFECORC\_Glycine\_max\_cold\_stressed\_leaves"  
 /note="Vector: Bluescript SK-/XhoI-EcoRI; Site 1: EcoRI; Site 2: XhoI; Plants were grown 12 days from seeds, treated at 20C for 3 days, then leaves were collected. Library was prepared using Unizap ZAP-cDNA synthesis kit / Packaged Gigapack III Gold."  
 298 a 207 c 158 g 165 t 3 others

BASE COUNT  
 ORIGIN

Alignment Scores:  
 Pred. No.: 1,36e-79 Length: 831  
 Score: 940.00 Matches: 177  
 Percent Similarity: 89.54% Conservative: 37  
 Best Local Similarity: 74.06% Mismatches: 25  
 Query Match: 73.90% Indels: 1  
 DB: 12 Gaps: 0

US-09-955-526-4 (1-248) x B6839316 (1-831)

QY 10 SerGlnSerAlaSerArgAsnArgTyrSerTyrAspSerLeuLysAsnPheArgGlnIle 29  
 Db 831 TCTTCTCTCTTCGAGAGCGCTGGAGTACGATCTCTCAAGATTCGCTGAGATC 772  
 QY 30 SerProLeuValGlnThrHisLeuLysGlnValTyrLeuThrLeuCysAlaLeuVal 49  
 Db 771 TCTCGCTGGTTCAGAAATCACATCAACAGGGGTTTATTTACGTTATGTTGGCTGGTG 712  
 QY 50 AlaSerAlaAlaGlyAlaTyrLeuHisIleLeuTrpAsnIleGlyGlyLeuLeuThr 69  
 Db 711 GCTGCTGCTGGAGCTTTCTCATGTTCTGTGGAACATTTGGGGTTTCTCACACG 652  
 QY 70 MetAlaCysMetGlySerMetValTrpLeuLeuSerAlaProProTyrGlnGluGlnLys 89  
 Db 651 TTGGCTTCCATTGGAAGCATGTTTG-TTGCTATCTACACCCCTGTTGAGAGCAAAAG 593  
 QY 90 ArgValAlaLeuLeuMetAlaAlaLeuPheGluGlyAlaSerIleGlyProLeuIle 109  
 Db 592 AGGTGTCTCTGTATGCTGCGCTTGGCTTGTTCAGGCGCTTCCATTGGACCTCTGAT 533  
 QY 110 GluLeuGlyIleAsnPheAspProSerIleValPheGlyAlaPheValGlyCysAlaVal 129  
 Db 532 GATTGGCTATGCTATGCTGCTAGCTTATGTTAGTGCAATTTGTGGCACTTCTTIG 473  
 QY 130 ValPheGlyCysPheSerAlaAlaMetLeuAlaArgArgGluTyrLeuTyrLeu 149  
 Db 472 GCTTTGTCTTCTCTGCGGACGCTTAGTTGCAAGCGCTAGGAGTACCTCTACCT 413  
 QY 150 GlyGlyLeuLeuSerSerGlyValSerLeuLeuPheTrpLeuHisPheAlaSerSerIle 169  
 Db 412 GTGGTTGCTCTCTCTGSGCTGCCAATTTATGTTGGTGGCACTTTGCTCTCTCTC 353  
 QY 170 PheGlyGlySerMetAlaPheLysPheGluLeuTyrPheGlyLeuValPheVal 189  
 Db 352 ITTGGGCTCAATTCGACTCTCAAGTTTGAGCTGTACTTTGGCTTTGGTGTGTG 293  
 QY 190 GlyTyrIleValPheAspThrGlnGluIleLeuGlyAlaHisLeuGlyAspMetAsp 209  
 Db 292 GGTACGTTATAGTACACTCAAGAAATTTATGAAGGGCTCACTTTTGGTCACTGGAT 233  
 QY 210 TyrValLysHisAlaLeuThrLeuPheThrAspPheGlyAlaValPheValArgIleLeu 229  
 Db 232 TATGGAAGCATGCAATTCATGCTGCTGATTTGGCGCAATTTTGTGCGAATTCCT 173  
 QY 230 IleIleMetLeuLysAsnAlaSerGluLysGluGlyLysLysLysArgArgAsn 248  
 Db 172 ATTATATGTTGAAGAATTCATCTGAGAGAATGAGAAGAGAGAGAGAT 116

RESULT 12  
 BQ856331  
 LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ856331 723 bp mRNA linear EST 14-AUG-2002  
 QGB2h05.yg.ab1 OG\_ABCDI lettuce salinas Lactuca sativa cDNA clone  
 QGB2h05, mRNA sequence.  
 BQ856331  
 BQ856331.1 GI:22241796  
 EST.  
 Lactuca sativa  
 Lactuca sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
 Cichorieae; Lactuca.  
 1 (bases 1 to 723)  
 Lin, H., van Damme, M., Lavelle, D., Chevaller, P., Ziegler, J., Ellison,  
 P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,  
 Church, S., Jackson, L. and Bradford, K.  
 Lettuce and Sunflower ESTs from the Compositae Genome Project  
 http://compgenomics.ucdavis.edu/  
 unpublished  
 Contact: Alexander Kozik [R.W.Michelmore]  
 Department of Vegetable Crops, R.W.Michelmore Lab  
 University of California at Davis (UCD)  
 Asmudson Hall, UCD, Davis, CA 95616, USA  
 Tel: 1-(530)-742-1742  
 Fax: 1-(530)-752-9659  
 Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]  
 belongs to contig OG\_CA\_Contig7943, see http://cgdb.ucdavis.edu/  
 for details.  
 Plate: QGB2 row: h column: 05.

FEATURES  
 Source

1..723  
 /organism="Lactuca sativa"  
 /mol\_type="mRNA"  
 /cultivar="Salinas"  
 /db\_xref="taxon:4236"  
 /clone="QGB2h05"  
 /lab\_host="E.coli"  
 /clone\_lib="OG\_ABCDI lettuce salinas"  
 /note="Vector: pBRCDNASFIAB; The library was constructed  
 from 10 different sources of RNA from a single genotype.  
 Separate cDNAs were generated using primers that  
 incorporated unique 5' and 3' tags to distinguish each  
 source of RNA. cDNAs were then pooled, size-fractionated,  
 directionally cloned into a custom medium-copy vector and  
 transformations made with four size classes to minimize  
 size bias. Details of each source of RNA and library  
 construction can be obtained at http://cgdb.ucdavis.edu/  
 TAG\_LIB-OG\_ABCDI lettuce salinas  
 TAG\_TISSUE=leaves dark grow  
 TAG\_SEQ=GTAGTCGGG"

BASE COUNT 159 a 174 c 141 g 249 t  
 ORIGIN

Alignment Scores:

Pred. No.: 5,55e-79 Length: 723  
 Score: 933.00 Matches: 180  
 Percent Similarity: 89.29% Conservative: 20  
 Best Local Similarity: 80.36% Mismatches: 21  
 Query Match: 73.35% Indels: 3  
 DB: 13 Gaps: 1

US-09-955-526-4 (1-248) x BQ856331 (1-723)

QY 1 MetGluGlyPheThrSerPhePheAspSerGln-----SerAlaSerArgAsnArgTyr 18  
 Db 50 ATGGAATCATCTCATCGTCTCTTCGATTCACAATCGCGATCGGCTTCTCCAAACAGCTGG 109  
 QY 19 SerTyrAspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLys 38  
 Db 110 ACCTACGATTCTCTCAAGATTTCCGTAATCTCCCTAGTTAGTTACAGATCATCTCAA 169

```

Qy 39 GlnValTyrLeuThrLeuCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHis 58
Db 170 CAGTTTACCTTCACACTATGCTTGCTCTCATGCACTCGAGTTGGGGCTTACCTTAC 229
Qy 59 IleLeuTrpAsnIleGlyGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrp 78
Db 230 ATCTATGGAACATCGGTGGCTTCTTAACACACTTCGGAACGTTGGGCTGCATGTTTGG 289

Qy 79 LeuLeuSerAlaProTyrGlnGluGln-LysArgValAlaLeuLeuMetAlaAla 98
Db 290 CTATCCGCCACTCCACAAATATCAAGAGCAAAAAGAGTCTCTATTAATGGCATCTTC 349
Qy 98 aLeuPheGluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProse 118
Db 350 TCTTCTCCAGGACCTCCATCGGTCTCTTAATCGACTTAGCCCATAGAAATTGACCCAA 409

Qy 118 rIleValPheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAla 138
Db 410 CATCTTGGTGAGCGGTTTCATGGGAACCTGCAATCGCATTTGCTTGTTCACAGAGCTGC 469
Qy 138 aMetLeuAlaArgArgArgGluTyrLeuTyrLeuGlyLeuLeuSerSerGlyValSe 158
Db 470 CATGTTACAGACGCGAGAGTATCTTATCTTGGAGGCTCTCTTCTTCTGTTGTTTC 529

Qy 158 rLeuLeuPheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLy 178
Db 530 AATCCTTTCTGTTTACATTTGCTCATCAATCTTTGGTGGCTCTGTTGCCCTTTTCAA 589
Qy 178 sPheGluLeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGl 198
Db 590 ATTTGAGTTGTACATTTGGGCTGTTGGTGTGTTGTTGGGTACATGTTGGTGTGACCCCA 649

Qy 198 uIleIleGluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeuThrLeuPh 218
Db 650 TATCATTTGAAGAGCTCATCTTGAGATTGGATTGGATTGGTAACATGCTCTACGCTTTT 709

Qy 218 eThrAspPhe 221
Db 710 CACTGATTTTC 719

RESULT 13
BG127849
LOCUS
DEFINITION
EST473495 tomato shoot/meristem Lycopersicon esculentum cDNA clone
ctof18E8 5' sequence, mRNA sequence.
ACCESSION
BG127849
VERSION
BG127849.1 GI:12628037
KEYWORDS
EST.
SOURCE
Lycopersicon esculentum (tomato)
ORGANISM
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 647)
van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,
Hansen,C., Ronning,C. and Tanksley,S.
Generation of ESTs from tomato shoot/meristem tissue
Unpublished
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
1. .647
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="ctof18E8"
/tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

```

```

/lab_host="SOLR"
/clone_lib="tomato shoot/meristem"
/clone_vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Small expanding leaves from the growing tip were
taken from greenhouse plants (4-6wks old TA496). Tissue
was immediately frozen in liquid nitrogen.

```

```

BASE COUNT      129 a      154 c      153 g      211 t
ORIGIN

Alignment Scores:
Pred. No.:      6,21e-79      Length:      647
Score:          932.00      Matches:      186
Percent Similarity: 98.41%      Conservatives: 0
Best Local Similarity: 98.41%      Mismatches: 1
Query Match:      73.27%      Indels:      2
DB:              10      Gaps:      0

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US-09-955-526-4 (1-248) x BG127849 (1-647)

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Qy 1 MetGluGlyPheThrSerPheAspSerGlnSerAlaSerArgAsnArgTrpSerTyr 20
Db 85 ATGGAAGGTTTCACATCGTTCTTCGACTCGCAATCTGCTCTCGCAACCGCTGGAGTTAT 144
Qy 21 AspSerLeuLysAsnPheArgGlnIleSerProLeuValGlnThrHisLeuLysGlnVal 40
Db 145 GATTCTCTCAAAAACCTTCCGCCAGACTCTCACTCTCGTCAAACTCATCTCAACAGAGTG 204
Qy 41 TyrLeuThrLeuCysCysAlaLeuValAlaSerAlaAlaGlyAlaTyrLeuHisIleLeu 60
Db 205 TACCTTACGCTATGCTGCTTTAGTGGCATCGGCTGCTGGGGCTTACCTTCACATTCTA 264
Qy 61 TrpAsnIleGlyLeuLeuThrThrMetAlaCysMetGlySerMetValTrpLeuLeu 80
Db 265 TSGAATATCGGTGGCTCTCTCACAAACATGCTTGCATGGGAAGCTGGTGTGGCTTCTC 324
Qy 81 SerAlaProTyrGlnGluGlnLysArgValAlaLeuLeuMetAlaAlaAlaLeuPhe 100
Db 325 TCAGTCTCTCTTATCAAGACGCAAAAAGGGTGGCTCTTCATGATGGCAGCTGCACCTTTT 384
Qy 101 GluGlyAlaSerIleGlyProLeuIleGluLeuGlyIleAsnPheAspProSerIleVal 120
Db 385 GAAGCGCGCTCTATTTGGTCTCTGATTGAGCTGGGCATTAACATTCGATCCAAGCATTTG 444
Qy 121 PheGlyAlaPheValGlyCysAlaValValPheGlyCysPheSerAlaAlaAlaMetLeu 140
Db 445 TTGGCGCTTTTGTAGGTGTGCTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 504
Qy 141 AlaArgArgArgGluTyrLeuTyrLeuGlyLeuLeuSerSerGlyValSerLeuLeu 160
Db 505 GCAAGCGCAGGAGTACTGTACTCGGGGCGCTTCTTTCATCTGCGCTCTCCCTTCTC 564
Qy 161 PheTrpLeuHisPheAlaSerSerIlePhe-GlyGlySerMet-AlaValPheLysPheG 180
Db 565 TTCTGGTGCATTTGTCATCTTCAATTTTGGTGGTTCATGGGCTCTTTTCAAGTTTG 624
Qy 180 luLeuTyrPheGlyLeuLeuVal 187
Db 625 AGTTGATTTTGGACTCTTTGGTG 647

```

```

RESULT 14
BU896719
LOCUS
DEFINITION
X044G02 Populus wood cDNA library Populus tremula x Populus
tremuloides cDNA 5 prime, mRNA sequence.
ACCESSION
BU896719
VERSION
BU896719.1 GI:24107926
KEYWORDS
EST.
SOURCE
Populus tremula x Populus tremuloides
ORGANISM
Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurossids I; Malpighiales; Salicaceae; Populus.
1 (bases 1 to 691)

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Db      409 ATTACAGCTTTGTGGGAACGTGGGTAGCCTTTGGATGTTCTCACTAGCAGCTATGTTG 468
QY      141 AlaArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyValSerLeuLeu 160
Db      469 GCCAGCGTAGAGAAATATCTTTACTTGGGTGGCTTGCITTCATCTGGCCCTTTCCATCCTT 528
QY      161 PheTrpLeuHisPheAlaSerSerIlePheGlyGlySerMetAlaValPheLysPheGlu 180
Db      529 CTATGGCTGCACCTTTGCATCCTCCATCTTTGGGGATCTGCAGCCCTCTTTAAATTTGAG 588
QY      181 LeuTyrPheGlyLeuLeuValPheValGlyTyrIleValPheAspThrGlnGluLeile 200
Db      589 CTGTACTTTGGGCTTCTGTGTGTGGGTATGTGGGTATGTGGTACACACCCAGGATATCATT 648
QY      201 GluLysAlaHisLeuGlyAspMetAspTyrValLysHisAlaLeu 215
Db      649 GAGAAAGCTCACCTTGGTGTATCTGGACTATGTGAGCAATTCCTG 693
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Search completed: September 22, 2003, 16:55:51  
Job time : 2072 secs